

85										90					95					
acc aac gac gat cct gaa cga ctc cgc ttt gaa ctg gaa aac gcc att	336																			
Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile																				
100 105 110																				
gac cag tat caa ccg gat gtc atc atc acc tct ggc ggt atc agc cac	384																			
Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His																				
115 120 125																				
ggt aaa ttt gag gtg ttt agg cag atc ctc gaa ggc acc ccg aac tcc	432																			
Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser																				
130 135 140																				
tgg ttt gga cat gtc gat cag cag cct ggc ggt cct caa ggc atc tcc	480																			
Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser																				
145 150 155 160																				
act ttt gct gaa act cct gtc att tca ctt ccc gga aat ccg att tcc	528																			
Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser																				
165 170 175																				
acc ttg gtg agt ttc aca ctt ttg gtc gcg cca gcg ctc aac cgc cag	576																			
Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln																				
180 185 190																				
ccg ctc cgc cac ctc gat gcc cgc atc acc gct ccg gtc cag ggc ttg	624																			
Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu																				
195 200 205																				
caa gac aat cgc gag caa ttc ctt cgc ggc acc atc agt tac cgc aac	672																			
Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn																				
210 215 220																				
ggg cca cgt cct cgc cac gcc tct cct ggg cac cag ttc cca cct gct	720																			
Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala																				
225 230 235 240																				
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Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp																				
245 250 255																				
tac ggt gga gga aaa cga cat cgt taagatttac ccattcaact aac	815																			
Tyr Gly Gly Gly Lys Arg His Arg																				
260																				

&lt;210&gt; 754

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 754

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Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser
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Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val
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<223> RXN02085
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Met Thr Ser Asn Phe  
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg	163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu	
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aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa	211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu	
25 30 35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
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tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
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atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat	355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	
70 75 80 85	
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
90 95 100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
150 155 160 165	
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883

Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly  
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027

Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075

Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
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 1123

Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171

Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
 1219

Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
 360 365 370

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 1267

Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
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cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315

Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363

Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
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cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411

Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
 1459

Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
 440 445 450



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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
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1027	
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
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Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	
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1123	
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330 335 340	
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1171	
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1219	
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
360 365 370	
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1267	
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
375 380 385	
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1315	

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc  
 2083  
 Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu  
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gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg  
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 Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val  
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tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt  
 2179  
 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly  
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ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc  
 2227  
 Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val  
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 Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala  
 710                    715                    720                    725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc  
 2323  
 Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
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&lt;210&gt; 756

&lt;211&gt; 745

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 756

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                     20                    25                    30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
                     35                    40                    45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
                     50                    55                    60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
                     65                    70                    75                    80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
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Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu

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	115						120					125			
Val	Pro	Glu	Leu	Ser	Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala
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Leu	Ile	Glu	Asp	Leu	Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg
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Pro	Val	Leu	Val	Gly	Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr
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Asp	Gly	Ser	Asn	Pro	Leu	Asp	His	Leu	Pro	Ala	Leu	Phe	Glu	Val	Tyr
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Glu	Arg	Leu	Ile	Lys	Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu
		195					200					205			
Pro	Ala	Leu	Val	Thr	Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg
	210					215					220				
Ala	Gly	Tyr	Thr	Thr	Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr
	225					230					235				240
Tyr	Phe	Gly	Ser	Gly	Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly
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Leu	Gly	Ala	Ile	Gly	Val	Asp	Leu	Val	Thr	His	Gly	Val	Thr	Glu	Leu
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Ala	Ala	Trp	Lys	Gly	Glu	Glu	Leu	Leu	Val	Ala	Gly	Ile	Val	Asp	Gly
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Arg	Asn	Ile	Trp	Arg	Thr	Asp	Leu	Cys	Ala	Ala	Leu	Ala	Ser	Leu	Lys
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	305					310					315				320
Leu	His	Val	Pro	Tyr	Thr	Leu	Glu	Ala	Glu	Asn	Ile	Glu	Pro	Glu	Val
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Arg	Asp	Trp	Leu	Ala	Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu
			340					345					350		
Leu	Ala	Asp	Ala	Leu	Ala	Gly	Asn	Ile	Asp	Ala	Ala	Ala	Phe	Asp	Ala
		355					360					365			
Ala	Ser	Ala	Ala	Ile	Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro
	370					375					380				
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Val	Thr	Leu	Gln	Glu	Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr
				405					410				415		
Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala
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Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
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 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
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 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
 485 490 495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
 500 505 510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
 515 520 525  
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr  
 530 535 540  
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 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile  
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 580 585 590  
 Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser  
 595 600 605  
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln  
 610 615 620  
 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser  
 625 630 635 640  
 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser  
 645 650 655  
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly  
 660 665 670  
 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala  
 675 680 685  
 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro  
 690 695 700  
 Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp  
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 <223> FRXA02085

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 Met Thr Ser Asn Phe  
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tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163  
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu  
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 Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu  
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 Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met  
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acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499  
 Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser  
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 Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu  
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
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gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
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1315	

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 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
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 ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
 1507  
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
 455 460 465  
 ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
 1555  
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
 470 475 480 485  
 gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
 1603  
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
 490 495 500  
 cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
 1651  
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
 505 510 515  
 cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
 1699  
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
 520 525 530  
 cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
 1747  
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
 535 540 545  
 ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
 1795  
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
 550 555 560 565  
 ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
 1843  
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
 570 575 580  
 atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg  
 1891  
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr

585

590

595

aga cgt cga taagcctgcc tacctgcagt ggt

1923

Arg Arg Arg

600

&lt;210&gt; 758

&lt;211&gt; 600

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 758

Met	Thr	Ser	Asn	Phe	Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly
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Ala	Lys	Arg	Glu	Leu	Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser
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Ile	Glu	Gly	Arg	Glu	Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr
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Ala	Ser	Asp	Ser	Leu	Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg
	50					55					60				

Ser	Tyr	Tyr	Asp	Ala	Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu
65					70					75					80

Pro	Glu	Arg	Phe	Asp	Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro
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Leu	Trp	Ile	Asp	Arg	Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu
			100					105					110		

Pro	Ala	Gln	Ala	Met	Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu
	115						120					125			

Val	Pro	Glu	Leu	Ser	Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala
	130					135					140				

Leu	Ile	Glu	Asp	Leu	Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg
145					150					155					160

Pro	Val	Leu	Val	Gly	Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr
				165				170						175	

Asp	Gly	Ser	Asn	Pro	Leu	Asp	His	Leu	Pro	Ala	Leu	Phe	Glu	Val	Tyr
			180					185					190		

Glu	Arg	Leu	Ile	Lys	Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu
	195						200					205			

Pro	Ala	Leu	Val	Thr	Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg
	210					215					220				

Ala	Gly	Tyr	Thr	Thr	Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr
225					230					235					240

Tyr	Phe	Gly	Ser	Gly	Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly
				245					250					255	



Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala  
 355 360 365  
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
 370 375 380  
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg  
 385 390 395 400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
 405 410 415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
 420 425 430  
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
 435 440 445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
 450 455 460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
 485 490 495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
 500 505 510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
 515 520 525  
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr  
 530 535 540  
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr  
 545 550 555 560  
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile  
 565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu  
 580 585 590

Leu Leu Pro Ala Thr Arg Arg Arg  
 595 600

<210> 759

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02086

<400> 759

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aacgatctca tcgaggctgg cgcgaagatc atccaggtgg atg agc ctg cga ttc 115  
 Met Ser Leu Arg Phe  
 1 5

gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163  
 Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln  
 10 15 20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211  
 Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp  
 25 30 35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259  
 Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile  
 40 45 50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307  
 Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala  
 55 60 65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355  
 Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu  
 70 75 80 85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403  
 Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro  
 90 95 100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451  
 Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val  
 105 110 115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499  
 Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg  
 120 125 130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547  
 Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala  
 135 140 145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600

Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
 150 155 160

aac

603

&lt;210&gt; 760

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 760

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys  
 1 5 10 15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala  
 20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu  
 35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
 50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
 85 90 95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
 100 105 110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
 115 120 125

Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val  
 130 135 140

Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
 145 150 155 160

&lt;210&gt; 761

&lt;211&gt; 1326

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1303)

&lt;223&gt; RXN02648

&lt;400&gt; 761

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gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg

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atc	agg	acc	act	cac	gtt	ggg	tcc	ttg	ccc	cgt	acc	cca	gag	cta	ctt	163	
Ile	Arg	Thr	Thr	His	Val	Gly	Ser	Leu	Pro	Arg	Thr	Pro	Glu	Leu	Leu		
				10					15					20			
gat	gca	aac	atc	aag	cgt	tct	aac	ggg	gag	att	ggg	gag	gag	gaa	ttc	211	
Asp	Ala	Asn	Ile	Lys	Arg	Ser	Asn	Gly	Glu	Ile	Gly	Glu	Glu	Glu	Phe		
				25					30					35			
ttc	cag	att	ctg	cag	tct	tct	gta	gat	gac	gtg	atc	aag	cgc	cag	gtt	259	
Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val	Ile	Lys	Arg	Gln	Val		
				40					45					50			
gac	ctg	ggg	atc	gac	atc	ctt	aac	gag	ggc	gaa	tac	ggc	cac	gtc	acc	307	
Asp	Leu	Gly	Ile	Asp	Ile	Leu	Asn	Glu	Gly	Glu	Tyr	Gly	His	Val	Thr		
				55					60					65			
tcc	ggg	gca	gtt	gac	ttc	ggg	gca	tgg	tgg	aac	tac	tcc	ttc	acc	cgc	355	
Ser	Gly	Ala	Val	Asp	Phe	Gly	Ala	Trp	Trp	Asn	Tyr	Ser	Phe	Thr	Arg		
				70					75					80			
ctg	ggc	gga	ctg	acc	atg	acc	gat	acc	gac	cgt	tgg	gca	agc	cag	gaa	403	
Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu		
				90					95					100			
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451	
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp		
				105					110					115			
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499	
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser		
				120					125					130			
ggc	atc	ttc	acc	ggg	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547	
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly		
				135					140					145			
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595	
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu		
				150					155					160			
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643	
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala		
				170					175					180			
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691	
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp		
				185					190					195			
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739	
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu		
				200					205					210			
tac	aag	atc	atc	acc	gat	gca	ggg	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787	
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro		
				215					220					225			
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835	
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys		
				230					235					240			
														245			

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883  
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala  
                   250                                  255                                  260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931  
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly  
                   265                                  270                                  275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979  
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile  
                   280                                  285                                  290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca  
 1027  
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala  
                   295                                  300                                  305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt  
 1075  
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu  
                   310                                  315                                  320                                  325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  
 1123  
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
                   330                                  335                                  340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  
 1171  
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
                   345                                  350                                  355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg  
 1219  
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
                   360                                  365                                  370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta  
 1267  
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
                   375                                  380                                  385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac  
 1313  
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
                   390                                  395                                  400

aacgagggtt gct  
 1326

<210> 762

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 762

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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
                   20                                  25                                  30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
                   35                                  40                                  45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
                   50                                  55                                  60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
                   65                                  70                                  75                                  80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
                                   85                                  90                                  95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
                   100                                  105                                  110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
                   115                                  120                                  125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
                   130                                  135                                  140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
                   145                                  150                                  155                                  160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
                                   165                                  170                                  175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
                   180                                  185                                  190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
                   195                                  200                                  205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
                   210                                  215                                  220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
                   225                                  230                                  235                                  240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
                                   245                                  250                                  255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
                   260                                  265                                  270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
                   275                                  280                                  285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
                   290                                  295                                  300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
                   305                                  310                                  315                                  320

Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
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Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg

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<211> 548
<212> DNA
<213> Corynebacterium glutamicum
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<222> (1)..(525)  
<223> FRXA02648
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agc	gtg	aag	gat	tac	ttg	gac	tgg	atc	ggc	aca	cgc	atc	gat	gcc	atc	96
Ser	Val	Lys	Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	
20				25				30								
aac	agt	gca	gtg	aag	ggc	ctt	cca	aag	gaa	cag	acc	cgc	ctg	cac	atc	144
Asn	Ser	Ala	Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	
35				40				45								
tgc	tgg	ggc	tct	tgg	cac	gga	cca	cac	gtc	act	gac	atc	cca	ttc	ggc	192
Cys	Trp	Gly	Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	
50				55				60								
gac	atc	att	ggc	gag	atc	ctg	cgc	gca	gag	gtc	ggc	ggc	ttc	tcc	ttc	240
Asp	Ile	Ile	Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	
65				70				75				80				
gaa	ggc	gca	tct	cct	cgt	cac	gca	cac	gag	tgg	cgt	gta	tgg	gaa	gaa	288
Glu	Gly	Ala	Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	
85				90				95								
aac	aag	ctt	cct	gaa	ggc	tct	gtt	atc	tac	cct	ggc	gtt	gtg	tct	cac	336
Asn	Lys	Leu	Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His	
100				105				110								
tcc	atc	aac	gct	gtg	gag	cac	cca	cgc	ctg	gtt	gct	gat	cgt	atc	gtt	384
Ser	Ile	Asn	Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg	Ile	Val	
115				120				125								
cag	ttc	gcc	aag	ctt	gtt	ggc	cct	gag	aac	gtc	att	gcg	tcc	act	gac	432
Gln	Phe	Ala	Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser	Thr	Asp	
130				135				140								

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480  
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525  
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

taagctagac aacgagggtt gct 548

<210> 764

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 764

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Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
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<210> 765

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658



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Met Ser Gln Asn Arg  
1 5  
atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
10 15 20  
gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
25 30 35  
ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
40 45 50  
gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
55 60 65  
tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg  
70 75 80 85  
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403  
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu  
90 95 100  
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp  
105 110 115  
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser  
120 125 130  
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547  
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly  
135 140 145  
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595  
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu  
150 155 160 165  
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643  
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala  
170 175 180  
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691  
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp  
185 190 195  
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739  
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
200 205 210  
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784

Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

<210> 766

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 766

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Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220

Gln Leu Asp Ala  
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<210> 767

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(490)

&lt;223&gt; RXA01516

&lt;400&gt; 767

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                                         Met Ala Asp Arg Ile
                                         1           5

gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
                        10                15                20

gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
                        25                30                35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
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tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
                        55                60                65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
                        70                75                80                85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
                        90                95                100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
                        105                110                115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
                        120                125                130

agttttgtcc atc 513

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&lt;210&gt; 768

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 768

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Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
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Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
                20                25                30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
                35                40                45

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Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile  
 50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser  
 65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val  
 85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val  
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Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser  
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Asn Ala  
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 <223> RXA01515

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 Met Asn Val Ser Ser  
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163  
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr  
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211  
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala  
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259  
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp  
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gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307  
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser  
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gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355  
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala  
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403  
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala  
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gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451  
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu  
                   105                  110                  115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499  
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val  
                   120                  125                  130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547  
 Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln  
                   135                  140                  145

gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595  
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp  
                   150                  155                  160                  165

gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643  
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile  
                   170                  175                  180

gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691  
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp  
                   185                  190                  195

cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739  
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile  
                   200                  205                  210

ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787  
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp  
                   215                  220                  225

cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835  
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala  
                   230                  235                  240                  245

gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883  
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His  
                   250                  255                  260

gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931  
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg  
                   265                  270                  275

agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975  
 Ser Gly Gly Thr His His Gly  
                   280

&lt;210&gt; 770

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 770

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly  
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Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile  
                   20                  25                  30

Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly  
           35                                  40                                  45  
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val  
           50                                  55                                  60  
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys  
           65                                  70                                  75                                  80  
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala  
                                   85                                  90                                  95  
 Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp  
                                   100                                  105                                  110  
 Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu  
           115                                  120                                  125  
 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly  
           130                                  135                                  140  
 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val  
           145                                  150                                  155                                  160  
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val  
                                   165                                  170                                  175  
 Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser  
                                   180                                  185                                  190  
 Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser  
           195                                  200                                  205  
 Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala  
           210                                  215                                  220  
 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp  
           225                                  230                                  235                                  240  
 Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp  
                                   245                                  250                                  255  
 Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val  
           260                                  265                                  270  
 Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly  
           275                                  280

&lt;210&gt; 771

&lt;211&gt; 859

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(859)

&lt;223&gt; RXA02024

&lt;400&gt; 771

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agcgcgtctc cacaattaag cagtggctac attaggtggt											atg	agt	tct	ttg	ccg	115
											Met	Ser	Ser	Leu	Pro	
											1				5	
gtc	atc	atg	gcc	atc	gtc	aat	cgc	acc	ccg	gat	tct	ttc	tat	gac	aag	163
Val	Ile	Met	Ala	Ile	Val	Asn	Arg	Thr	Pro	Asp	Ser	Phe	Tyr	Asp	Lys	
				10					15					20		
ggg	gcg	aca	ttt	gag	gac	acc	gct	gcg	cta	aac	agg	gca	gcg	gag	gtc	211
Gly	Ala	Thr	Phe	Glu	Asp	Thr	Ala	Ala	Leu	Asn	Arg	Ala	Ala	Glu	Val	
				25					30					35		
att	gaa	caa	ggc	gcc	ggc	att	gtc	gat	atc	ggg	ggg	gtg	aaa	gcc	ggc	259
Ile	Glu	Gln	Gly	Ala	Gly	Ile	Val	Asp	Ile	Gly	Gly	Val	Lys	Ala	Gly	
				40					45					50		
ccg	ggg	gat	ttc	gtg	tcg	gcg	gag	gaa	gag	atc	gac	cgc	gtg	gtg	cca	307
Pro	Gly	Asp	Phe	Val	Ser	Ala	Glu	Glu	Glu	Ile	Asp	Arg	Val	Val	Pro	
				55					60					65		
atc	atc	gct	gcg	gtg	cga	gaa	cgt	ttt	cct	gac	att	gat	att	tct	gtt	355
Ile	Ile	Ala	Ala	Val	Arg	Glu	Arg	Phe	Pro	Asp	Ile	Asp	Ile	Ser	Val	
				70					75					80		
gat	acc	tgg	cgg	gcg	tcg	gtg	gct	gat	gtc	gca	gtg	gcg	cat	gga	gca	403
Asp	Thr	Trp	Arg	Ala	Ser	Val	Ala	Asp	Val	Ala	Val	Ala	His	Gly	Ala	
				90					95					100		
acg	ctg	atc	aat	gac	act	tgg	gcc	ggc	cat	gat	cat	gag	ttg	gtg	cag	451
Thr	Leu	Ile	Asn	Asp	Thr	Trp	Ala	Gly	His	Asp	His	Glu	Leu	Val	Gln	
				105					110					115		
gta	gca	ggg	cag	cac	aag	gtg	ggg	tat	gtc	tgc	tcg	cac	acc	ggc	ggg	499
Val	Ala	Gly	Gln	His	Lys	Val	Gly	Tyr	Val	Cys	Ser	His	Thr	Gly	Gly	
				120					125					130		
gtg	att	cca	aga	acg	cga	cca	tat	cgg	gtg	cat	ttc	gat	gac	atc	gtg	547
Val	Ile	Pro	Arg	Thr	Arg	Pro	Tyr	Arg	Val	His	Phe	Asp	Asp	Ile	Val	
				135					140					145		
gcc	gat	gta	att	acg	gag	acc	acc	aaa	ttg	gca	gag	caa	gct	gtt	cgt	595
Ala	Asp	Val	Ile	Thr	Glu	Thr	Thr	Lys	Leu	Ala	Glu	Gln	Ala	Val	Arg	
				150					155					160		
gcc	ggg	gtg	cca	gag	gaa	cgg	gtg	ttt	att	gat	ccc	acc	cat	gat	ttc	643
Ala	Gly	Val	Pro	Glu	Glu	Arg	Val	Phe	Ile	Asp	Pro	Thr	His	Asp	Phe	
				170					175					180		
ggg	aaa	aac	acc	ttc	cac	gga	ctg	gag	ctt	tta	cga	cgg	atc	gat	gag	691
Gly	Lys	Asn	Thr	Phe	His	Gly	Leu	Glu	Leu	Leu	Arg	Arg	Ile	Asp	Glu	
				185					190					195		
gtg	gtt	gcc	acg	ggc	tgg	ccg	gtg	ctg	atg	gcc	ttg	agt	aat	aag	gat	739
Val	Val	Ala	Thr	Gly	Trp	Pro	Val	Leu	Met	Ala	Leu	Ser	Asn	Lys	Asp	
				200					205					210		
ttc	att	ggg	gaa	act	ttg	gaa	agg	ggc	gtc	gat	aag	cgt	gtt	gct	ggc	787
Phe	Ile	Gly	Glu	Thr	Leu	Glu	Arg	Gly	Val	Asp	Lys	Arg	Val	Ala	Gly	
				215					220					225		

acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt 835  
 Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe  
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cgc gtg cat gaa gtt gcg gaa acc 859  
 Arg Val His Glu Val Ala Glu Thr  
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<210> 772

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

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 35 40 45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile  
 50 55 60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp  
 65 70 75 80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala  
 85 90 95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp  
 100 105 110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys  
 115 120 125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His  
 130 135 140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala  
 145 150 155 160

Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp  
 165 170 175

Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu  
 180 185 190

Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala  
 195 200 205

Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp  
 210 215 220

Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg  
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Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr



245

250

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 <222> (101)..(661)  
 <223> RXA01719

<400> 773

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                                   Met Asn Ile Ile Ile
                                   1 5
ctt gct ggt ggc gag ggt aaa cgc atg ggt ggg gtg gat aag gct gct 163
Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly Val Asp Lys Ala Ala
                                   10 15 20
gtg gcg gtg gat ggt cgc acg ctg ctg gat atc ctg ctt tca cag ctg 211
Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile Leu Leu Ser Gln Leu
                                   25 30 35
gat cca gaa gat gac gtc gtg gtg gtt tcc ccc gcg atc atc gac gga 259
Asp Pro Glu Asp Asp Val Val Val Ser Pro Ala Ile Ile Asp Gly
                                   40 45 50
atc acg act gtc tgc gag gaa cct ccg ctt ggc ggg ccg gtc gcg gga 307
Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly Gly Pro Val Ala Gly
                                   55 60 65
atc gag gca ggg ctg aat tct ttt gag cac gcc cat gaa ttc act gcg 355
Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala His Glu Phe Thr Ala
                                   70 75 80 85
att ctt gcc gtg gac gcg cct tat tct gca gcg atg ctg ccc cta ctt 403
Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala Met Leu Pro Leu Leu
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cag gca cag att ggc aaa gcc gat gtg gcc gta acc ctt gct gcc gat 451
Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val Thr Leu Ala Ala Asp
                                   105 110 115
ggc tgg gta caa ccg ttg tgc gcg ctg tgg aga agt ggc agc cta gaa 499
Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg Ser Gly Ser Leu Glu
                                   120 125 130
gcg gtg att cac agc ctg ggc gag act aga aat cga ccg gca aaa gcg 547
Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn Arg Pro Ala Lys Ala
                                   135 140 145
tta ctg aag caa gcg gga cac att gtg gaa gtg ggt ggc gat ggc act 595
Leu Leu Lys Gln Ala Gly His Ile Val Glu Val Gly Gly Asp Gly Thr
                                   150 155 160 165
gaa aaa gac tac gat acg gtg gct gaa ctg gag gta ttg ggc aac gta 643

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Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu Val Leu Gly Asn Val  
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acg ctc cct aaa gcc cac tgatgagaaa cgtgagctct gct 684  
 Thr Leu Pro Lys Ala His  
 185

<210> 774  
 <211> 187  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 774  
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 Leu Leu Ser Gln Leu Asp Pro Glu Asp Asp Val Val Val Val Ser Pro  
 35 40 45  
 Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly  
 50 55 60  
 Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala  
 65 70 75 80  
 His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala  
 85 90 95  
 Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val  
 100 105 110  
 Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg  
 115 120 125  
 Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn  
 130 135 140  
 Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val  
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<220>  
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 <223> RXA01720

&lt;400&gt; 775

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ctatatattt gagtgtttat tgtcgaaaaa ggggtttcaa gtg gca cag caa cgc 115  
Val Ala Gln Gln Arg  
1 5

agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163  
Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu  
10 15 20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211  
Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu  
25 30 35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259  
Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser  
40 45 50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307  
Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly  
55 60 65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355  
Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro  
70 75 80 85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403  
Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro  
90 95 100

gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc 451  
Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr  
105 110 115

aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag 499  
Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu  
120 125 130

cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa 547  
Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys  
135 140 145

gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act 595  
Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr  
150 155 160 165

gtg tcg acg gtg att tca gtt ggc cat gac act gta aaa gcc cat cct 643  
Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro  
170 175 180

tgc cct cgg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga 691  
Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly  
185 190 195

aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag 739  
Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu  
200 205 210

cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat 787  
Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His Phe His Ser Asp Asp

215	220	225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg			835
Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala			
230	235	240	245
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg			883
Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val			
250	255		260
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att			931
Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile			
265	270		275
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca			979
Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala			
280	285		290
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt			
1027			
Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe			
295	300		305
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg			
1075			
Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg			
310	315		320
ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac cgg			
1123			
Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg			
330	335		340
gcg ctg aag gcg cgg gag ggc ccc gta ttg gcg ata ccg gtg gcg att			
1171			
Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile			
345	350		355
gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg			
1219			
Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met			
360	365		370
gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg			
1267			
Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser			
375	380		385
att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg			
1309			
Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met			
390	395		400
taaatagaata tcatcattct tgc			
1332			

&lt;210&gt; 776

&lt;211&gt; 403

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 776

Val Ala Gln Gln Arg Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp  
 1 5 10 15  
 Ser Val Ala Pro Leu Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His  
 20 25 30  
 Pro Leu Ser His Leu Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro  
 35 40 45  
 Lys Phe Thr Asn Ser Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp  
 50 55 60  
 Ile His Gly Ser Gly Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro  
 65 70 75 80  
 Ala Gly Ser Ala Pro Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val  
 85 90 95  
 Met Thr Gly Gly Pro Val Pro Ser Thr Asn Lys Asp Met Ile Val Val  
 100 105 110  
 Pro Val Glu Leu Thr Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu  
 115 120 125  
 Ile Thr Ile Asn Glu Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala  
 130 135 140  
 Gly Glu His Leu Lys Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala  
 145 150 155 160  
 Phe Asp Ala Gly Thr Val Ser Thr Val Ile Ser Val Gly His Asp Thr  
 165 170 175  
 Val Lys Ala His Pro Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp  
 180 185 190  
 Glu Leu Asn Gln Gly Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro  
 195 200 205  
 Met Leu Val Ala Glu Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His  
 210 215 220  
 Phe His Ser Asp Asp Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys  
 225 230 235 240  
 Pro Ala Glu Val Ala Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala  
 245 250 255  
 Gly Ala Phe Asp Val Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe  
 260 265 270  
 Glu Phe Phe Pro Ile Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly  
 275 280 285  
 Gln Trp Gly Asp Ala Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala  
 290 295 300  
 Ala Trp Val Ser Phe Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu  
 305 310 315 320

Gly Gly Gly Lys Arg Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala  
325 330 335

Leu Arg Ser Asn Arg Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala  
340 345 350

Ile Pro Val Ala Ile Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala  
355 360 365

His Arg Ser His Met Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala  
370 375 380

Leu Val Thr Ser Ser Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu  
385 390 395 400

Gly Arg Met

<210> 777

<211> 1237

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (2) .. (1207)

<223> RXS03223

<400> 777

tcca	gag	cca	gtg	cgt	att	gct	att	gca	gag	gca	ctg	ggg	ttg	atg	tgc	49
Pro	Glu	Pro	Val	Arg	Ile	Ala	Ile	Ala	Glu	Ala	Leu	Gly	Leu	Met	Cys	
1				5					10					15		

gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 97  
Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala  
20 25 30

gcg att gat ggt tat gcg gtt cga gca gtc gat gtc ggc ggc gag aag 145  
Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys  
35 40 45

tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc 193  
Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro  
50 55 60

gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag 241  
Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln  
65 70 75 80

cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt 289  
Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu  
85 90 95

gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt ggc cgc aaa cga 337  
Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg  
100 105 110

gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa 385  
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu

115	120	125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val 130 135 140			433
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys 145 150 155 160			481
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala 165 170 175			529
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp 180 185 190			577
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp 195 200 205			625
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu 210 215 220			673
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly 225 230 235 240			721
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu 245 250 255			769
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val 260 265 270			817
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu 275 280 285			865
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg 290 295 300			913
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val 305 310 315 320			961
gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1009 Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys 325 330 335			
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1057 Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr 340 345 350			

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg  
1105

Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu  
355 360 365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc  
1153

Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val  
370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa  
1201

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln  
385 390 395 400

ggt cga tagttcgatg cgtaatgcac cgtcaggtcc  
1237

Gly Arg

<210> 778

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 778

Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys  
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Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala  
20 25 30

Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys  
35 40 45

Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro  
50 55 60

Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln  
65 70 75 80

Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu  
85 90 95

Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg  
100 105 110

Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu  
115 120 125

Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val  
130 135 140

Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys  
145 150 155 160

Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala  
165 170 175

Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp



180										185										190										
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp															
		195						200						205																
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu															
	210					215						220																		
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly															
	225				230					235					240															
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu															
				245					250					255																
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val															
		260						265					270																	
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu															
	275					280						285																		
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg															
	290					295					300																			
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val															
	305				310					315				320																
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys															
				325					330					335																
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr															
		340						345					350																	
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu															
	355					360						365																		
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val															
	370					375					380																			
Thr	Glu	Ile	Arg	Pro	Gly	Asp	Val	Val	Asp	Val	Ile	Phe	Leu	Ala	Gln															
	385				390					395					400															

Gly Arg

&lt;210&gt; 779

&lt;211&gt; 1229

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1206)

&lt;223&gt; FRXA01970

&lt;400&gt; 779

cca	gag	cca	gtg	cgt	att	gct	att	gca	gag	gca	ctg	ggt	ttg	atg	tgc	48
Pro	Glu	Pro	Val	Arg	Ile	Ala	Ile	Ala	Glu	Ala	Leu	Gly	Leu	Met	Cys	
1				5				10					15			

gcg	gaa	gag	gtt	caa	gct	agt	cgt	gct	ttg	ccg	ggt	ttc	gcg	caa	gca	96
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala	
			20					25					30			
gcg	att	gat	ggg	tat	gcg	gtt	cga	gca	gtc	gat	gtc	ggc	ggc	gag	aag	144
Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys	
		35					40					45				
tcg	ttt	agc	cag	caa	ctg	ccg	gtt	gct	cct	ccg	gaa	aaa	tcc	ctg	ccc	192
Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro	
	50					55					60					
gtg	gtg	ggg	gaa	gta	gct	gcg	ggg	tct	cag	cag	ccg	ttg	cgc	ctg	cag	240
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln	
65					70					75					80	
cct	aaa	caa	gca	gtc	atg	gtc	cac	acc	ggg	gcg	cca	ctg	ccg	atg	ctt	288
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu	
			85						90					95		
gcg	gat	gcg	gtg	ctg	ccc	atg	gcg	tgg	tca	gat	cgt	ggc	cgc	aaa	cga	336
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg	
			100					105					110			
gta	acc	gcg	cag	cga	cct	gtg	cgc	tct	ggc	gag	ttt	gtg	cgc	aaa	gaa	384
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu	
		115					120					125				
ggc	gat	gac	atc	caa	ccg	gga	gac	atc	gca	gtc	agc	gcc	ggc	gcg	gtc	432
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val	
	130					135					140					
tta	ggc	cct	gcc	caa	att	ggg	ttg	ctc	gca	gct	gtt	ggg	cgc	tcc	aaa	480
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys	
145				150						155					160	
gtg	ttg	gtg	tac	cca	cgc	cca	cgc	atg	tcg	gtt	atc	tcc	gta	ggc	gct	528
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala	
			165						170					175		
gaa	ctt	gtt	gat	att	gat	cgc	cag	cca	ggc	ctc	ggc	cag	gtt	tat	gat	576
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp	
			180				185					190				
gtc	aat	tcc	tat	tct	ctg	gct	gcc	gcc	ggg	agg	gaa	gcg	ggc	gca	gat	624
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp	
		195					200					205				
gtg	tac	cgc	tac	ggc	att	gct	gcc	ggg	gaa	cct	cgt	cgc	atc	aaa	gag	672
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu	
	210					215					220					
atc	att	gaa	tcc	cag	atg	ctg	cgc	tcg	gaa	atc	atc	gtc	atc	acc	gga	720
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly	
225					230					235					240	
gct	gtt	ggc	ggg	gct	ggg	tca	gct	ggc	gtg	cgc	cag	gtt	ctc	aac	gag	768
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu	
				245					250					255		
cta	ggc	gat	atc	gac	acc	gaa	cgc	gtc	gca	atg	cac	ccc	ggg	tct	gtc	816
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val	

260	265	270	
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg			864
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu			
275	280	285	
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc			912
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg			
290	295	300	
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt			960
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val			
305	310	315	320
gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa			
1008			
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys			
	325	330	335
ggg ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac			
1056			
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr			
	340	345	350
ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg			
1104			
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu			
	355	360	365
gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc			
1152			
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val			
	370	375	380
aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa			
1200			
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln			
385	390	395	400
ggg cga tagttcgatg cgtaatgcac cgt			
1229			
Gly Arg			

&lt;210&gt; 780

&lt;211&gt; 402

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 780

Pro	Glu	Pro	Val	Arg	Ile	Ala	Ile	Ala	Glu	Ala	Leu	Gly	Leu	Met	Cys
1				5					10					15	

Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala
			20					25					30		

Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys
		35					40					45			

Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln 65 70 75 80		
Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu 85 90 95		
Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg 100 105 110		
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu 115 120 125		
Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val 130 135 140		
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys 145 150 155 160		
Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala 165 170 175		
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp 180 185 190		
Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp 195 200 205		
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu 210 215 220		
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly 225 230 235 240		
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu 245 250 255		
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val 260 265 270		
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu 275 280 285		
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg 290 295 300		
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val 305 310 315 320		
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys 325 330 335		
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr 340 345 350		
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu 355 360 365		
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val 370 375 380		

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln  
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Gly Arg

<210> 781  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA02629

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 Met Ser Lys Asp Pro  
 1 5  
 ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163  
 Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp  
 10 15 20  
 gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211  
 Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His  
 25 30 35  
 atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259  
 Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val  
 40 45 50  
 gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307  
 Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Leu Glu  
 55 60 65  
 tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355  
 Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser  
 70 75 80 85  
 cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403  
 Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu  
 90 95 100  
 gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451  
 Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro  
 105 110 115  
 gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499  
 Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln  
 120 125 130  
 gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547  
 Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val  
 135 140 145

tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595  
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu  
 150 155 160 165  
  
 gct gag tct cgt tcg gca att cgt gat ggc atg gca act ctg aca ccg 643  
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro  
 170 175 180  
  
 ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685  
 Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr Ser Val Val  
 185 190 195  
  
 tgagttgggtc ggggtgtgagt aga 708

&lt;210&gt; 782

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 782

Met Ser Lys Asp Pro Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg  
 1 5 10 15  
  
 Val Pro Leu Pro Asp Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr  
 20 25 30  
  
 Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu  
 35 40 45  
  
 Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr  
 50 55 60  
  
 Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val  
 65 70 75 80  
  
 Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val  
 85 90 95  
  
 Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro  
 100 105 110  
  
 Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val  
 115 120 125  
  
 Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala  
 130 135 140  
  
 Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr  
 145 150 155 160  
  
 Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met  
 165 170 175  
  
 Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr  
 180 185 190  
  
 Ser Val Val  
 195

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<220>  
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 <222> (101)..(379)  
 <223> RXA02318

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cagtaagcgc atgtgcgcca ttttaaggca agatggggcc atg aat tcg ctt ttc 115  
 Met Asn Ser Leu Phe  
 1 5

gac gtc tcc cca cac tgg tcc tcc gcc aac gcc aag ctc acc gca cat 163  
 Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala Lys Leu Thr Ala His  
 10 15 20

ttt aac acc gga aaa ttc tcc act ggc atg aaa ttt gtc aac ctc att 211  
 Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys Phe Val Asn Leu Ile  
 25 30 35

gcc gac tcc gca gaa gaa gcc aac cac cac ccc gat atc ctt ctc acc 259  
 Ala Asp Ser Ala Glu Glu Ala Asn His His Pro Asp Ile Leu Leu Thr  
 40 45 50

tat ggt ttt gtg gaa atc acc ctc acc agc cac gat gtg ggt gag ata 307  
 Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His Asp Val Gly Glu Ile  
 55 60 65

acc gac cgt gat gtc gcc cta gca aaa gtc atc gac gcc cac gcc aag 355  
 Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile Asp Ala His Ala Lys  
 70 75 80 85

acc ttg gcc att tcg gca gag gct taagggtaaa gattatgagc aac 402  
 Thr Leu Ala Ile Ser Ala Glu Ala  
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<210> 784  
 <211> 93  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 784  
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Lys Leu Thr Ala His Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys  
 20 25 30

Phe Val Asn Leu Ile Ala Asp Ser Ala Glu Glu Ala Asn His His Pro  
 35 40 45

Asp Ile Leu Leu Thr Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His  
 50 55 60

Asp Val Gly Glu Ile Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile

65	70	75	80
Asp Ala His Ala Lys Thr Leu Ala Ile Ser Ala Glu Ala			
85	90		
<p>&lt;210&gt; 785          &lt;211&gt; 600          &lt;212&gt; DNA          &lt;213&gt; Corynebacterium glutamicum</p> <p>&lt;220&gt;          &lt;221&gt; CDS          &lt;222&gt; (101)..(577)          &lt;223&gt; RXA01517</p> <p>&lt;400&gt; 785</p>			
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gttccaggaa atccatggct gctggaagga gcaacgccta atg cat gca gtt ttg	115		
Met His Ala Val Leu			
1 5			
tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg	163		
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val			
10 15 20			
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca	211		
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser			
25 30 35			
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg	259		
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val			
40 45 50			
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc	307		
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly			
55 60 65			
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg	355		
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly			
70 75 80 85			
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa	403		
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu			
90 95 100			
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct	451		
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala			
105 110 115			
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat	499		
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp			
120 125 130			
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat	547		
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp			
135 140 145			
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat	597		
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile			



150 155

gca

600

&lt;210&gt; 786

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 786

Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala  
 1 5 10 15

Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln  
 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu  
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu  
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg  
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile  
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu  
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu  
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His  
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile  
 145 150 155

&lt;210&gt; 787

&lt;211&gt; 609

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(586)

&lt;223&gt; RXN01304

&lt;400&gt; 787

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tgaaaaagg gattaattac cccacttga ggagaaattg atg ccc gca cag aac 115  
 Met Pro Ala Gln Asn  
 1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163  
 Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser

	10	15	20	
gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag				211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln				
	25	30	35	
gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt				259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe				
	40	45	50	
gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc				307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg				
	55	60	65	
gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg				355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr				
	70	75	80	85
ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg				403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met				
	90	95	100	
acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta				451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu				
	105	110	115	
tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc				499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu				
	120	125	130	
atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg				547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly				
	135	140	145	
gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagatttt				596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu				
	150	155	160	
ttgcttatcg acg				609

&lt;210&gt; 788

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 788

Met Pro Ala Gln Asn Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser  
 1 5 10 15

Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala  
 20 25 30

Val Asp Leu Leu Gln Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val  
 35 40 45

Val Glu Glu Gly Phe Glu Pro Val His Gln Glu Leu Val Lys Ala Leu  
 50 55 60

Ala Arg Arg Asp Arg Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly  
 65 70 75 80

[illegible]

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<211> 1281
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1258)
<223> RXS02556
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gtagaaatta gcccatgaag catggaaagg cgaaaacccc															115
<div> <div>Leu</div> <div>Ile</div> <div>Val</div> <div>Ser</div> <div>Thr</div> </div> <div>15</div>															5
cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg															163
<div> <div>Gln</div> <div>Pro</div> <div>Ile</div> <div>Thr</div> <div>Asp</div> <div>Arg</div> <div>Ser</div> <div>Ala</div> <div>Leu</div> <div>Ser</div> <div>Ala</div> <div>Glu</div> <div>His</div> <div>Ala</div> <div>Glu</div> <div>Val</div> </div> <div>10</div> <div>15</div> <div>20</div>															
atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg															211
<div> <div>Ile</div> <div>Lys</div> <div>Ala</div> <div>Thr</div> <div>Leu</div> <div>Pro</div> <div>Leu</div> <div>Val</div> <div>Gly</div> <div>Gly</div> <div>Lys</div> <div>Ile</div> <div>Asn</div> <div>Glu</div> <div>Ile</div> <div>Thr</div> </div> <div>25</div> <div>30</div> <div>35</div>															
ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct															259
<div> <div>Pro</div> <div>Val</div> <div>Phe</div> <div>Tyr</div> <div>Asn</div> <div>Lys</div> <div>Met</div> <div>Phe</div> <div>Ala</div> <div>Ala</div> <div>His</div> <div>Pro</div> <div>Glu</div> <div>Leu</div> <div>Ile</div> <div>Ala</div> </div> <div>40</div> <div>45</div> <div>50</div>															
aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg															307
<div> <div>Asn</div> <div>Thr</div> <div>Phe</div> <div>Asn</div> <div>Arg</div> <div>Gly</div> <div>Asn</div> <div>Gln</div> <div>Lys</div> <div>Gln</div> <div>Gly</div> <div>Asp</div> <div>Gln</div> <div>Gln</div> <div>Lys</div> <div>Ala</div> </div> <div>55</div> <div>60</div> <div>65</div>															
ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat															355
<div> <div>Leu</div> <div>Ala</div> <div>Ala</div> <div>Ser</div> <div>Ile</div> <div>Ala</div> <div>Thr</div> <div>Phe</div> <div>Ala</div> <div>Thr</div> <div>Met</div> <div>Leu</div> <div>Val</div> <div>Thr</div> <div>Pro</div> <div>Asp</div> </div> <div>70</div> <div>75</div> <div>80</div> <div>85</div>															
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg															403
<div> <div>Ala</div> <div>Pro</div> <div>Asp</div> <div>Pro</div> <div>Val</div> <div>Gln</div> <div>Leu</div> <div>Leu</div> <div>Ser</div> <div>Arg</div> <div>Ile</div> <div>Gly</div> <div>His</div> <div>Lys</div> <div>His</div> <div>Val</div> </div> <div>90</div> <div>95</div> <div>100</div>															

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg	451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu	
105 110 115	
ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct	499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro	
120 125 130	
gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg	547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu	
135 140 145	
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc	595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly	
150 155 160 165	
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca	643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala	
170 175 180	
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca	691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro	
185 190 195	
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag	739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln	
200 205 210	
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att	787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile	
215 220 225	
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta	835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val	
230 235 240 245	
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt	883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val	
250 255 260	
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc	931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly	
265 270 275	
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac	979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp	
280 285 290	
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg	
1027	
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val	
295 300 305	
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa	
1075	
Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu	
310 315 320 325	
atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att	
1123	
Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile	

330 335 340  
 cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag  
 1171  
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys  
 345 350 355  
 aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta  
 1219  
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val  
 360 365 370  
 aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca  
 1268  
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 375 380 385  
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<210> 790  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys  
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 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  
 35 40 45  
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly  
 50 55 60  
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met  
 65 70 75 80  
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  
 85 90 95  
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile  
 100 105 110  
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu  
 115 120 125  
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile  
 130 135 140  
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn  
 145 150 155 160  
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys  
 165 170 175  
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu

180										185					190				
Val	Ala	Pro	Glu	Pro	Gly	Gln	Tyr	Thr	Ser	Ile	Gly	Val	Val	Leu	Asp				
		195					200					205							
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	210					215					220								
Thr	Glu	Tyr	Arg	Ile	Ala	Val	Glu	Asp	Asn	Gly	Glu	Val	Ser	Gly	Phe				
225					230					235					240				
Leu	Arg	Asp	Arg	Val	Ser	Val	Gly	Asp	Lys	Ile	Glu	Ala	Thr	Ile	Ala				
			245						250					255					
Ala	Gly	Asp	Leu	Val	Leu	Asn	Lys	Asp	Thr	Asn	Pro	Val	Val	Leu	Ile				
		260						265					270						
Ser	Gln	Gly	Ile	Gly	Ser	Thr	Pro	Met	Val	Gly	Met	Leu	Ala	Gly	Met				
	275						280					285							
Asn	Pro	Glu	Arg	Asp	Val	Val	Val	Leu	His	Ala	Asp	Gln	Ala	Glu	Ser				
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Thr	Tyr	Ala	Gln	Val	Glu	Glu	Val	Gln	Gly	Leu	Val	Glu	Lys	Leu	Pro				
305					310					315					320				
Lys	Ala	Ala	Phe	Glu	Ile	Phe	Tyr	Arg	Asp	Asn	Asp	Gln	Trp	Leu	Glu				
			325						330					335					
Val	Ala	Gly	Arg	Ile	Pro	Ser	Gly	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Gly				
			340					345					350						
Val	Glu	Phe	Leu	Lys	Asn	Val	Arg	Glu	Gln	Ile	Glu	Ala	Leu	Asp	Glu				
	355						360					365							
Gln	Pro	Arg	Asp	Val	Asn	Phe	Glu	Leu	Phe	Ala	Pro	Asn	Asp	Trp	Leu				
	370					375					380								
Ile	Ser																		
385																			

&lt;210&gt; 791

&lt;211&gt; 990

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(967)

&lt;223&gt; RXS02560

&lt;400&gt; 791

ttggggcgaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60

ggaacttcta	agagcagtgg	aatgaaataa	tccggtgctg	atg	cag	ggc	aac	tcg	115
				Met	Gln	Gly	Asn	Ser	
				1				5	

ctt	aat	ctg	gca	gac	aac	agc	gag	aga	aag	aag	ccc	atg	ccg	tca	cca	163
Leu	Asn	Leu	Ala	Asp	Asn	Ser	Glu	Arg	Lys	Lys	Pro	Met	Pro	Ser	Pro	

10								15				20				
gga	gaa	ctt	tta	gcc	gcc	cgc	tac	gga	caa	cct	gca	acc	tgg	acg	cca	211
Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro	
25				30				35								
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt	259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val	
40				45				50								
cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att	307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile	
55				60				65								
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att	355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile	
70				75				80				85				
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg	403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly	
90				95				100								
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg	451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu	
105				110				115								
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa	499
Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu	
120				125				130								
gat	ctc	cca	aca	ggg	gct	ctt	gat	tat	ctc	gat	gag	gcc	gcg	tgg	ggg	547
Asp	Leu	Pro	Thr	Gly	Ala	Leu	Asp	Tyr	Leu	Asp	Glu	Ala	Ala	Trp	Gly	
135				140				145								
ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag	595
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu	
150				155				160				165				
tca	ctt	gga	ttg	gga	acg	ctc	tat	ttg	ggt	tcg	gtg	cgc	aac	gat	gcg	643
Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala	
170				175				180								
gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc	691
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val	
185				190				195								
gtg	ggc	ttg	gaa	atg	ggg	cat	gcg	gat	ccg	cct	gaa	cct	gcc	gga	att	739
Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile	
200				205				210								
aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc	787
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr	
215				220				225								
gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act	835
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr	
230				235				240				245				
tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg	883
Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	Ser	Lys	Gln	Thr	Ala	
250				255				260								

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931  
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu  
                   265                                  270                                  275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977  
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg  
                   280                                  285

attatggacg cct 990

<210> 792

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 792

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys  
   1                                  5                                  10                                  15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro  
                                   20                                  25                                  30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His  
                                   35                                  40                                  45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp  
   50                                  55                                  60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser  
   65                                  70                                  75                                  80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg  
                                   85                                  90                                  95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln  
                                   100                                  105                                  110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala  
                                   115                                  120                                  125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp  
                                   130                                  135                                  140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala  
   145                                  150                                  155                                  160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser  
                                   165                                  170                                  175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro  
                                   180                                  185                                  190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro  
                                   195                                  200                                  205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His  
                                   210                                  215                                  220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp



225	230	235	240
Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp			
	245	250	255
Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr			
	260	265	270
Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu			
	275	280	285

Arg

&lt;210&gt; 793

&lt;211&gt; 1425

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1402)

&lt;223&gt; RXA00382

&lt;400&gt; 793

aaaacactat tgaccacccc aatcgctgtt gagagtttgt aaagttcgac tgtcaacgag 60

ctggattggc ttcacagatt gaattaatac aatgacgcac atg aca tcg tcc aat	115
Met Thr Ser Ser Asn	
1 5	

acg gct cga tcc gca gag tgg ttt gaa aag gct cag aag ctc acc cct	163
Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala Gln Lys Leu Thr Pro	
10 15 20	

ggg ggt gtg aat tct cct gtt cgc gct ttc ggt tca gtt ggc gga caa	211
Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly Ser Val Gly Gly Gln	
25 30 35	

gcc cgt ttc atc gaa aaa gct cac ggt tca acg ctg atc gat gtg gac	259
Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr Leu Ile Asp Val Asp	
40 45 50	

gga aat gaa tac gtt gac ctg gtc tgt tct tgg ggc ccc atg ctg atg	307
Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp Gly Pro Met Leu Met	
55 60 65	

ggg cac gct cac cca gca gtg gtc gag gct gtg cag aag gcc gtc gtg	355
Gly His Ala His Pro Ala Val Val Glu Ala Val Gln Lys Ala Val Val	
70 75 80 85	

gat ggt ctt tct ttc ggc gct ccc acc atc ggt gag gtt gag ttg gcc	403
Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly Glu Val Glu Leu Ala	
90 95 100	

caa gat atc gtc aag cgc act tct gtg gag gaa gtc cgc ctg gtc aac	451
Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu Val Arg Leu Val Asn	
105 110 115	

tcc ggc act gag gcc acc atg tcg gcg gtt cgt ctg gcg cgc ggt tac	499
---	-----

Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg Leu Ala Arg Gly Tyr	
120 125 130	
act cag cgt tcc aag att ttg aag ttt gag ggc tgc tac cac ggc cac	547
Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly Cys Tyr His Gly His	
135 140 145	
gtc gat gcg ctg ctc gca tct gct ggt tct ggt gtc gca act ttc gct	595
Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly Val Ala Thr Phe Ala	
150 155 160 165	
ctg cct gat tcc cca ggc atc acc ggc gct cag act tct gac act att	643
Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln Thr Ser Asp Thr Ile	
170 175 180	
gtt gtt cct tac aac gac att gaa gcc gtg cgc aac gct ttt gcg gag	691
Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg Asn Ala Phe Ala Glu	
185 190 195	
tac cca ggc gag atc gcc tgc atc atc gca gag gca gcc ggt ggc aac	739
Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu Ala Ala Gly Gly Asn	
200 205 210	
atg ggc acc gtc gct cca aag gac aac ttt aac gac aag ctt ctc gcg	787
Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn Asp Lys Leu Leu Ala	
215 220 225	
atc gct cac gct gac ggc gcg ctg ctg atc ctc gat gaa gtc atg acc	835
Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu Asp Glu Val Met Thr	
230 235 240 245	
ggc ttc cgc acc tct tac cgt ggc tgg ttc ggc gta gac aag gtt gcc	883
Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly Val Asp Lys Val Ala	
250 255 260	
gct gac ctg gtc acc ttc ggc aag gtc gtc tcc ggc ggc cta cct gcc	931
Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser Gly Gly Leu Pro Ala	
265 270 275	
gca gcg ttt ggc ggc aag gct gaa atc atg aac atg ctg gcc cca cag	979
Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn Met Leu Ala Pro Gln	
280 285 290	
ggc ccc gtc tac caa gca ggc aca ctg tcc ggc aac ccg gtt gcg gtc	
1027	
Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly Asn Pro Val Ala Val	
295 300 305	
gca gct ggt cgg gca tcg ctt aag ctt gcc gac gaa tcc ctc tac aca	
1075	
Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp Glu Ser Leu Tyr Thr	
310 315 320 325	
acc atc aac gcc aac gca gat cgt ctc cac ggt ttg atc tct gat gcc	
1123	
Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly Leu Ile Ser Asp Ala	
330 335 340	
tta acc cac gaa ggc gta gcc cac cac att cag cgt gcc tca aac atg	
1171	
Leu Thr His Glu Gly Val Ala His His Ile Gln Arg Ala Ser Asn Met	

345                                      350                                      355  
 ctg tct atc cgt ttt gca gaa ggt gag ggc cac aac ttc tct gat atg  
 1219  
 Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His Asn Phe Ser Asp Met  
           360                                      365                                      370  
  
 aag gca gcc gac atc ttc cgc ttc gca ccg ttc ttc cac act ttg ctg  
 1267  
 Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe Phe His Thr Leu Leu  
           375                                      380                                      385  
  
 gac aac ggc gtc tac gca cca cca agc gtt ttc gaa acc tgg ttt gtg  
 1315  
 Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe Glu Thr Trp Phe Val  
 390                                      395                                      400                                      405  
  
 tct tcc gct ctc acg gac gat gat ttc tcc aag atc gag cag gca ctc  
 1363  
 Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys Ile Glu Gln Ala Leu  
                                     410                                      415                                      420  
  
 aag ccc gcc gca cgt gca gca gca gaa gcg aag gca tca tgacgcaaac  
 1412  
 Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys Ala Ser  
                                     425                                      430  
  
 cattgtccat cta  
 1425

&lt;210&gt; 794

&lt;211&gt; 434

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 794

Met Thr Ser Ser Asn Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala  
   1                                    5                                    10                                    15  
  
 Gln Lys Leu Thr Pro Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly  
                                     20                                    25                                    30  
  
 Ser Val Gly Gly Gln Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr  
                                     35                                    40                                    45  
  
 Leu Ile Asp Val Asp Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp  
   50                                    55                                    60  
  
 Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val  
   65                                    70                                    75                                    80  
  
 Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly  
                                     85                                    90                                    95  
  
 Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu  
                                     100                                    105                                    110  
  
 Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg  
                                     115                                    120                                    125

Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly  
 130 135 140  
 Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly  
 145 150 155 160  
 Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln  
 165 170 175  
 Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg  
 180 185 190  
 Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu  
 195 200 205  
 Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn  
 210 215 220  
 Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu  
 225 230 235 240  
 Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly  
 245 250 255  
 Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser  
 260 265 270  
 Gly Gly Leu Pro Ala Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn  
 275 280 285  
 Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly  
 290 295 300  
 Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp  
 305 310 315 320  
 Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly  
 325 330 335  
 Leu Ile Ser Asp Ala Leu Thr His Glu Gly Val Ala His His Ile Gln  
 340 345 350  
 Arg Ala Ser Asn Met Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His  
 355 360 365  
 Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe  
 370 375 380  
 Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe  
 385 390 395 400  
 Glu Thr Trp Phe Val Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys  
 405 410 415  
 Ile Glu Gln Ala Leu Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys  
 420 425 430  
 Ala Ser

<210> 795  
 <211> 1233  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1210)  
 <223> RXA00156

<400> 795

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tttttatgca atatcaacca aaagttggta cgatcctcat atg aat gaa cgc aca 115  
 Met Asn Glu Arg Thr  
 1 5

tcg gat gca ttt gac gcc ctc ctt gtg ctc tcc ttc ggt ggt ccc gaa 163  
 Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser Phe Gly Gly Pro Glu  
 10 15 20

ggg cac gag gag gtt cgt ccg ttt ttg gag aat gtc act cac gga agg 211  
 Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg  
 25 30 35

ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259  
 Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His  
 40 45 50

ttc ggt ggt atc agc ccc atc aat gcg ctg aac agg gaa att atc gcc 307  
 Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn Arg Glu Ile Ile Ala  
 55 60 65

aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat 355  
 Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr  
 70 75 80 85

ttt ggt aac cgc aac tgg aag ccg ttt gat aat gag gcc gct gaa caa 403  
 Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln  
 90 95 100

atg gct gat gac ggc gtg aaa aac gcg ctg gtg ttg gca act tcc gct 451  
 Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala  
 105 110 115

tgg ggt ggc tac tcc ggt tgt cgg cag tac cag gaa gat att cag ggc 499  
 Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln Glu Asp Ile Gln Gly  
 120 125 130

atg atc aag cac ctg gag tct cag ggg cag tcg atc acg ttc acc aag 547  
 Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys  
 135 140 145

ctg cgt cag ttc tac gat cac cct cgt ttt gtc tcc acc atg gct caa 595  
 Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val Ser Thr Met Ala Gln  
 150 155 160 165

ttg gtt cag gat tcc tac gcg aag ctt ccc gat gag ctg cga gat gag 643  
 Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu  
 170 175 180

gcg cgt ctg gtc ttc acc gcg cac tcc att cca ctg act gcg gac aat 691  
 Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro Leu Thr Ala Asp Asn  
 185 190 195

gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739  
 Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys  
 200 205 210

gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787  
 Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp  
 215 220 225

gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag 835  
 Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu  
 230 235 240 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883  
 Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys  
 250 255 260

gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931  
 Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val  
 265 270 275

att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac 979  
 Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn  
 280 285 290

atg gtg gtc gag cgt gtc gct acc gtt ggc ccc acc gat gaa ttc gca  
 1027  
 Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala  
 295 300 305

gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc  
 1075  
 Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile  
 310 315 320 325

gag cgc ctt gga aag ctg cca gca cgc gga agt tcc gtc aac ggc gca  
 1123  
 Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala  
 330 335 340

ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg  
 1171  
 Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg  
 345 350 355

gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat  
 1220  
 Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala Ala Asn  
 360 365 370

agtccctcgc aaa  
 1233

&lt;210&gt; 796

&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 796

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Met Asn Glu Arg Thr Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser
 1              5              10              15

Phe Gly Gly Pro Glu Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn
          20              25              30

Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala
      35              40              45

Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
 50              55              60

Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His
 65              70              75              80

Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn
          85              90              95

Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val
      100              105              110

Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln
      115              120              125

Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser
      130              135              140

Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val
      145              150              155              160

Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp
          165              170              175

Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro
      180              185              190

Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr
      195              200              205

Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly
      210              215              220

Val Ser Asp Phe Asp Val Val Trp Gln Ser Arg Ser Gly Ser Pro His
      225              230              235              240

Thr Pro Trp Leu Glu Pro Asp Ile Val Asp His Ala Val Glu Leu Asn
          245              250              255

Glu Lys Gly Gln Lys Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser
      260              265              270

Asp His Met Glu Val Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu
      275              280              285

Ala Glu Lys Arg Asn Met Val Val Glu Arg Val Ala Thr Val Gly Pro
      290              295              300

Thr Asp Glu Phe Ala Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu
      305              310              315              320

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Leu Lys Arg Val Ile Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser  
325 330 335

Ser Val Asn Gly Ala Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys  
340 345 350

His Lys Thr Ala Arg Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala  
355 360 365

Ala Asn  
370

<210> 797

$\langle 211 \rangle$  810

<212> DNA

<213> Corynebacterium glutamicum

<220>

&lt;221&gt; CDS

<222> (101) .. (787)

<223> RXA00624

<400> 797

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caacaggacg acaacggccg gacatgcgac aataacaatgc atg tcc ggc cgt ctt    115
               Met Ser Gly Arg Leu
                   1               5

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ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac 163  
 Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp  
 10 15 20

agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt 211  
Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu  
25 30 35

gtc gca ccc cgc atc gat ggg gac tgg cgt ctc gcc aaa gac aaa ggg 259  
Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly  
40 45 50

acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307  
Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile  
55 60 65

ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355  
Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala  
70 75 80 85

aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403  
Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg  
90 95 100

caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451  
Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg  
105 110 115

tgg aga atg tca gaa ggc acc ttc gcg gta ctc cca gaa ttt gat ttc 499  
 Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe



120	125	130	
aac gtc gcc gcc tcg acc agg gga tta cat aac ctc gac acc ggc gaa			547
Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu			
135	140	145	
ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca			595
Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala			
150	155	160	165
aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa			643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu			
	170	175	180
aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac			691
Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn			
	185	190	195
cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat			739
Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp			
	200	205	210
ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc			787
Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala			
	215	220	225
tagttgggga gggtcggggc acc			810

&lt;210&gt; 798

&lt;211&gt; 229

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 798

Met Ser Gly Arg Leu Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr			
1	5	10	15
Arg Ser Ala Ala Asp Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile			
	20	25	30
Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu			
	35	40	45
Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg			
	50	55	60
Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg			
	65	70	75
Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu			
	85	90	95
Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile			
	100	105	110
Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu			
	115	120	125
Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn			
	130	135	140

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu  
 145 150 155 160  
 Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val  
 165 170 175  
 Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala  
 180 185 190  
 Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala  
 195 200 205  
 Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala  
 210 215 220  
 Ala Ala Gln Leu Ala  
 225

<210> 799  
 <211> 956  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
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 <222> (1)..(933)  
 <223> RXA00306

<400> 799  
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 1 5 10 15  
 gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96  
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30  
 gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144  
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45  
 cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192  
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu  
 50 55 60  
 aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240  
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala  
 65 70 75 80  
 gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288  
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly  
 85 90 95  
 tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336  
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr  
 100 105 110  
 gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384  
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu

115	120	125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag			432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys			
130	135	140	
ggt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa			480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu			
145	150	155	160
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag			528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln			
165	170	175	
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc			576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg			
180	185	190	
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc			624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg			
195	200	205	
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat			672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp			
210	215	220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc			720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg			
225	230	235	240
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc			768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser			
245	250	255	
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg			816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu			
260	265	270	
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac			864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn			
275	280	285	
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg			912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu			
290	295	300	
ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag			956
Pro Ala Asp Leu Leu Asp Ser			
305	310		
<210> 800			
<211> 311			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 800			
Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro			
1	5	10	15
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val			

20										25										30										
Val	Gly	Pro	Pro	Glu	Ile	Gly	His	Val	Tyr	Arg	Asp	Ser	Gly	Met	Asp															
35								40				45																		
Leu	Asp	Gly	Ala	Thr	Ala	Leu	Val	Val	Lys	Glu	Ala	Cys	Ala	His	Leu															
50				55				60																						
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala															
65		70				75				80																				
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly															
				85		90				95																				
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr															
100				105				110																						
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu															
115				120				125																						
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys															
130				135				140																						
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu															
145		150				155				160																				
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln															
				165		170				175																				
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg															
180				185				190																						
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg															
195				200				205																						
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp															
210				215				220																						
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg															
225		230				235				240																				
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser															
				245				250				255																		
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu															
260				265				270																						
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn															
275				280				285																						
Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu															
290		295				300																								
Pro	Ala	Asp	Leu	Leu	Asp	Ser																								
305		310																												

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<210> 801
<211> 1263
<212> DNA
<213> Corynebacterium glutamicum
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1240)

&lt;223&gt; RXA00884

&lt;400&gt; 801

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caattaatca tgtatagggg gcaggcacta ggcttggggc atg tca gtt ttt ggt 115
                                         Met Ser Val Phe Gly
                                         1           5

gtg tat att cat gtg ccg ttt tgt tca act cgg tgc ggt tat tgc gat 163
Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg Cys Gly Tyr Cys Asp
                        10                        15                        20

ttc aac acc tat act gct ggg gaa tta ggt agt act gca ggc ccg gac 211
Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser Thr Ala Gly Pro Asp
                        25                        30                        35

acc tat ctt gac tcg ttg gaa gtt gag ttg gag atg gct gtg gct tcg 259
Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu Met Ala Val Ala Ser
                        40                        45                        50

ctg gat aat cct cgg cag gcg gaa act atc ttt att ggc ggg ggt acc 307
Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe Ile Gly Gly Gly Thr
                        55                        60                        65

ccg tcg ttg att ggt gcg gac ggt ttg gcc agg gtt ttg ggg gct gtg 355
Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg Val Leu Gly Ala Val
                        70                        75                        80                        85

cgc aat act ttt ggc att gcg gat ggt gcg gaa gtc acc acg gag tcc 403
Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu Val Thr Thr Glu Ser
                        90                        95                        100

aat ccg gag tct acc tcg cct gag ttt ttt gat ggc ctg cgt gag gcg 451
Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp Gly Leu Arg Glu Ala
                        105                        110                        115

ggc tac aac agg att tcg tta ggg atg cag tcg gcg tcg tca agc gtt 499
Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser Ala Ser Ser Ser Val
                        120                        125                        130

ttg aag gtg ctg gac cgc acg cac acc cca ggg cgc ccg gtg gcg gcg 547
Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly Arg Pro Val Ala Ala
                        135                        140                        145

gcc aag gag gca cgt gag gcg ggg ttt gag cat gtc aat ttg gac atg 595
Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His Val Asn Leu Asp Met
                        150                        155                        160                        165

att tat ggc acg ccg aca gag acc gat gat gat gtc cgc aag acg ctg 643
Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp Val Arg Lys Thr Leu
                        170                        175                        180

aat gcg gtg ctc gaa gcg aac gtg gat cac gtg tct gcc tat tcc ttg 691
Asn Ala Val Leu Glu Ala Asn Val Asp His Val Ser Ala Tyr Ser Leu
                        185                        190                        195

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atc gtg aaa gat ggc acg gcg atg gcg cgc aag gtg cac aag ggc gag 739  
 Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys Val His Lys Gly Glu  
 200 205 210

ctg cca gcg ccg gac gag gat gtc tac gct gat cgt ttt gag ctt atc 787  
 Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp Arg Phe Glu Leu Ile  
 215 220 225

gac gct cgc ctg cgc tca gct ggt ttc gat tgg tac gag gtg tcc aac 835  
 Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp Tyr Glu Val Ser Asn  
 230 235 240 245

tgg gcg aaa ccc ggc gga gaa tgc aag cac aac atg ggc tat tgg gtc 883  
 Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn Met Gly Tyr Trp Val  
 250 255 260

gac ggc gac tgg tgg ggc gcg ggc ccg ggc gcg cac tcg cac atc ggc 931  
 Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala His Ser His Ile Gly  
 265 270 275

gac cgc cgc ttc tac aac atc aag cac cca gcg cgt tac tcc gcg cag 979  
 Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln  
 280 285 290

att gcg gcc ggc gag ctg ccc att aag gaa aca gag cgg ctg acg gcg  
 1027  
 Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr Glu Arg Leu Thr Ala  
 295 300 305

gaa gat cac cac acc gag cgc gtc atg ctt ggt ttg cgc ctg aaa caa  
 1075  
 Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln  
 310 315 320 325

ggc gtg ccg ctg aac ctt ttc gca ccc gca gcg cgc ccg gtc atc gac  
 1123  
 Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp  
 330 335 340

cgt cat atc gca ggc ggc ctg ctg cac gtc aat gcg ctg ggc aac ctg  
 1171  
 Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu  
 345 350 355

gcg gtg acc gat gcg gga cgt ttg ctt gcc gac ggc atc atc gcc gac  
 1219  
 Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp  
 360 365 370

att ttg ctt agt gaa gaa gac taaatattta gtaggggttac aga  
 1263  
 Ile Leu Leu Ser Glu Glu Asp  
 375 380

&lt;210&gt; 802

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 802

Met Ser Val Phe Gly Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg  
 1 5 10 15  
 Cys Gly Tyr Cys Asp Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser  
 20 25 30  
 Thr Ala Gly Pro Asp Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu  
 35 40 45  
 Met Ala Val Ala Ser Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe  
 50 55 60  
 Ile Gly Gly Gly Thr Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg  
 65 70 75 80  
 Val Leu Gly Ala Val Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu  
 85 90 95  
 Val Thr Thr Glu Ser Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp  
 100 105 110  
 Gly Leu Arg Glu Ala Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser  
 115 120 125  
 Ala Ser Ser Ser Val Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly  
 130 135 140  
 Arg Pro Val Ala Ala Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His  
 145 150 155 160  
 Val Asn Leu Asp Met Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp  
 165 170 175  
 Val Arg Lys Thr Leu Asn Ala Val Leu Glu Ala Asn Val Asp His Val  
 180 185 190  
 Ser Ala Tyr Ser Leu Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys  
 195 200 205  
 Val His Lys Gly Glu Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp  
 210 215 220  
 Arg Phe Glu Leu Ile Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp  
 225 230 235 240  
 Tyr Glu Val Ser Asn Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn  
 245 250 255  
 Met Gly Tyr Trp Val Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala  
 260 265 270  
 His Ser His Ile Gly Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala  
 275 280 285  
 Arg Tyr Ser Ala Gln Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr  
 290 295 300  
 Glu Arg Leu Thr Ala Glu Asp His His Thr Glu Arg Val Met Leu Gly  
 305 310 315 320  
 Leu Arg Leu Lys Gln Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala

	325		330		335
Arg Pro Val Ile Asp Arg His Ile Ala Gly Gly Leu Leu His Val Asn					
	340		345		350
Ala Leu Gly Asn Leu Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp					
	355		360		365
Gly Ile Ile Ala Asp Ile Leu Leu Ser Glu Glu Asp					
	370		375		380

<210> 803  
 <211> 522  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(499)  
 <223> RXN02503

<400> 803  
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ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115  
 Met Thr Leu Lys Ile  
 1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163  
 Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg  
 10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211  
 Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr  
 25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259  
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly  
 40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307  
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp  
 55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355  
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg  
 70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc 403  
 Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile  
 90 95 100

gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt 451  
 Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly  
 105 110 115

ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc 499  
 Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro  
 120 125 130



tgacctggag attctccac tgc

522

&lt;210&gt; 804

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 804

Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln  
 1 5 10 15

Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu  
 20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu  
 35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His  
 50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr  
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Ser  
 85 90 95

Arg Glu Ala Leu Ile Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro  
 100 105 110

Glu Arg Arg Lys Gly Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala  
 115 120 125

Gln Gly Asn Pro Pro  
 130

&lt;210&gt; 805

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(535)

&lt;223&gt; FRXA02503

&lt;400&gt; 805

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ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115  
 Met Thr Leu Lys Ile  
 1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163  
 Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg  
 10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211  
 Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr  
 25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259  
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly  
           40                          45                          50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307  
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp  
           55                          60                          65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355  
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg  
           70                          75                          80                          85

ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403  
 Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr  
                           90                          95                          100

cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451  
 Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg  
                           105                          110                          115

tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499  
 Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg  
           120                          125                          130

cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545  
 Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His  
           135                          140                          145

atgggcaagg tca 558

&lt;210&gt; 806

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 806

Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln  
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Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu  
           20                          25                          30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu  
           35                          40                          45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His  
           50                          55                          60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr  
           65                          70                          75                          80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa  
                           85                          90                          95

Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa  
           100                          105                          110

Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln  
           115                          120                          125

Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys  
 130 135 140

His  
 145

<210> 807  
 <211> 1245  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1222)  
 <223> RXA00377

<400> 807  
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 Val Trp Leu Leu Phe  
 1 5  
 cta aat tgg gat aaa tgg ggc aag att gag cgc atg tct gct ctt act 163  
 Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg Met Ser Ala Leu Thr  
 10 15 20  
 att cca gct gcg cgt cgc acg cta aat aac gcg ccc att att gat gcc 211  
 Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala Pro Ile Ile Asp Ala  
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 gct aat ggc aag acc ccg act cgc act ccg gtg tgg ttt atg cgc cag 259  
 Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val Trp Phe Met Arg Gln  
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 Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val Arg Glu Gly Ile Ser  
 55 60 65  
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 Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu Ala Glu Ile Thr Leu  
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 Gln Pro Val Arg Arg His Asp Val Asp Ala Ala Ile Leu Phe Ser Asp  
 90 95 100  
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 Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly Val Glu Ile Val Ala  
 105 110 115  
 ggt cgt gga cct gtg ttg gat gcg ccg gtg cgg agc cgt ggg gat gtg 499  
 Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg Ser Arg Gly Asp Val  
 120 125 130  
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 Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro Glu Val Glu Gln Gly  
 135 140 145

att ggc atc att ttg gat gag ttg tct gat tct cag gcg ttg att ggt	595
Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly	
150 155 160 165	
ttt gct ggt gcg ccg ttt acg ttg gcg agt tac ttg gtt gag ggt ggt	643
Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly	
170 175 180	
cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct	691
Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro	
185 190 195	
gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat	739
Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn	
200 205 210	
tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt	787
Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe	
215 220 225	
gat tcg tgg gct ggg ttc ctc act gag cgt gat tac acc gag ttc gtg	835
Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val	
230 235 240 245	
ttg ccg tat tcc act gag att ttg gag gaa gtg ggc aag tac cag ctg	883
Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu	
250 255 260	
cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg	931
Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met	
265 270 275	
agc aag gct ggc tca gag gtc atg ggt gtg gat tgg cgg gtg ccg ttg	979
Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu	
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gat aag gct gcg gag cgt att gct gcg gta tca ggt cct aag gtg ttg	1027
Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser Gly Pro Lys Val Leu	
295 300 305	
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Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala Gly Arg Ala Pro Leu	
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Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala Gln Thr Ala Val Asp	
330 335 340	
gca ggt cat gca acg ggc cat atc ttt aac ctt ggt cat ggt gtg ctt	1171
Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu	
345 350 355	
cct aat acg gtg gcg gaa gat att act gaa gcc gtc tcc atc att cat	1219
Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala Val Ser Ile Ile His	
360 365 370	

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 1245  
 Ser

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 808  
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                     20                    25                    30  
 Pro Ile Ile Asp Ala Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val  
                     35                    40                    45  
 Trp Phe Met Arg Gln Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val  
     50                    55                    60  
 Arg Glu Gly Ile Ser Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu  
     65                    70                    75                    80  
 Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala  
                     85                    90                    95  
 Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly  
                     100                    105                    110  
 Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg  
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 Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro  
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 Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser  
     145                    150                    155                    160  
 Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr  
                     165                    170                    175  
 Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met  
                     180                    185                    190  
 Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val  
                     195                    200                    205  
 Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp  
     210                    215                    220  
 Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp  
     225                    230                    235                    240  
 Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val  
                     245                    250                    255  
 Gly Lys Tyr Gln Leu Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu

260	265	270
Leu Leu Gly Ala Met Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp		
275	280	285
Trp Arg Val Pro Leu Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser		
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Gly Pro Lys Val Leu Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala		
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Gly Arg Ala Pro Leu Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala		
325	330	335
Gln Thr Ala Val Asp Ala Gly His Ala Thr Gly His Ile Phe Asn Leu		
340	345	350
Gly His Gly Val Leu Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala		
355	360	365
Val Ser Ile Ile His Ser		
370		

&lt;210&gt; 809

&lt;211&gt; 681

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(658)

&lt;223&gt; RXN02504

&lt;400&gt; 809

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                               Val Gly Thr Ser Ala
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Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile
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ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc 211
Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met Gly Lys Val Thr Ser
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ggg gaa ctc gat gct gtg atg ctc gcc tac gca ggc ctc acc cgc gtc 259
Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val
          40          45          50
ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg 307
Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met
          55          60          65
ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac 355
Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp
          70          75          80          85

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 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly  
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tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499  
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly  
                     120                    125                    130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547  
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp  
                     135                    140                    145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595  
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu  
                     150                    155                    160                    165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643  
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu  
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ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681  
 Leu Gly Asp Arg Ser  
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&lt;210&gt; 810

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 810

Val Gly Thr Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg  
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Pro Asp Leu Glu Ile Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met  
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Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala  
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Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp  
                     50                    55                    60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu  
                     65                    70                    75                    80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met  
                     85                    90                    95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn  
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Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu  
                     115                    120                    125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala  
                     130                    135                    140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala  
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Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala  
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Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser  
 180 185

&lt;210&gt; 811

&lt;211&gt; 561

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(538)

&lt;223&gt; FRXA02504

&lt;400&gt; 811

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 Met Leu Val Met Leu  
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gcc tac gca ggc ctc acc cgc gtc ggc atg cag gac cgc gca acg gaa 163  
 Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu  
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gtt ttc gac gcc gac atc atc atg ccc gcc ccc gca cag ggc gca ctt 211  
 Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu  
 25 30 35

gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac 259  
 Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn  
 40 45 50

atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc 307  
 Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr  
 55 60 65

gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac 355  
 Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His  
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gcc acc ttg gac gcc tac tcc gcc gac acc atg act ctc acc gcc ggc 403  
 Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly  
 90 95 100

gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt 451  
 Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly  
 105 110 115

gac ggc gcc cgc cca gaa gag ctc gcc gag ctc gtt gca caa cag ctt 499  
 Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu  
 120 125 130

atc gac gcc gga gcc gcc aat ttg ctc gcc gac cgc agc taattagggc 548



Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser  
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561

<210> 812

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 812

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Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr  
 35 40 45

Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe Val Ser Ala  
 50 55 60

Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala  
 65 70 75 80

Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met  
 85 90 95

Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val  
 100 105 110

Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu  
 115 120 125

Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp  
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Arg Ser  
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<210> 813

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1426)

<223> RXN01162

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 Met Tyr Ile Val Gly  
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Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp	
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Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val	
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Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro	
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Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly	
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Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile	
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Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu	
90 95 100	
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg	451
Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu	
105 110 115	
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Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp	
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Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met	
135 140 145	
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Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys	
150 155 160 165	
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga	643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly	
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Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln	
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Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr	
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Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser	
215 220 225	
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat	835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His	
230 235 240 245	
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc	883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg	

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Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp																														
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Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met																														
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1027																														
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1075																														
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val																														
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1123																														
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser																														
330	335	340																												
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta																														
1171																														
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val																														
345	350	355																												
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc																														
1219																														
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly																														
360	365	370																												
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct																														
1267																														
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro																														
375	380	385																												
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag																														
1315																														
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys																														
390	395	400	405																											
ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc																														
1363																														
Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg																														
410	415	420																												
atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act																														
1411																														
Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr																														
425	430	435																												
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1449																														
Pro Glu Ala Val Asn																														
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 814

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Thr	His	Phe	Ala	Val	Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr
		35					40					45			
Ala	Pro	Arg	Ala	Pro	Ala	Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr
	50					55					60				
Asp	Gly	Phe	Glu	Gly	Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg
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Ala	Ser	Val	Val	Ile	Gly	Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp
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Ala	Ile	Lys	Ala	Glu	Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro
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Leu	Ala	Ser	Gly	Asp	Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val
	130					135					140				
His	Val	Leu	Gly	Met	Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser
145					150					155					160
Ala	Ser	Leu	Ala	Cys	Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg
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Val	Val	Tyr	Leu	Gly	Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile
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Glu	Ser	Gly	Ala	Gln	Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr
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Leu	Thr	Val	Leu	Ser	Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln
225					230					235					240
Gly	Thr	Ala	Ser	His	Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile
				245					250					255	
Ala	Val	Gly	Ala	Arg	Thr	Ala	Met	Pro	Lys	Pro	His	Phe	Glu	Gly	Asp
			260					265					270		
Val	Ser	Asn	Glu	Asp	Leu	Arg	Ala	Leu	Thr	Val	Ala	Ala	Leu	Glu	Pro
		275					280					285			
Thr	Gln	Gly	Gln	Met	Leu	Trp	Thr	Phe	Gly	Asp	Ile	Gly	Ala	Ala	Leu

290	295	300
Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser 305	310	315 320
Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly 325	330	335
Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys 340	345	350
Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile 355	360	365
Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp 370	375	380
Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu 385	390	395 400
Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile 405	410	415
Ile Lys His Ile Arg Ile Asp Asp Thr Asp Val His Gln Trp Arg Val 420	425	430
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&lt;210&gt; 815

&lt;211&gt; 1345

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1345)

&lt;223&gt; FRXA01162

&lt;400&gt; 815

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Met Tyr Ile Val Gly  
1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163  
Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp  
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tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta 211  
Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val  
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gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca 259  
Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro  
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gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg 307  
Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly

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gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu 90 95 100			403
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu 105 110 115			451
ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp 120 125 130			499
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met 135 140 145			547
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys 150 155 160 165			595
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly 170 175 180			643
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln 185 190 195			691
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr 200 205 210			739
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser 215 220 225			787
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His 230 235 240 245			835
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acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp 265 270 275			931
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met 280 285 290			979
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta 1027 Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			

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 Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val  
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 1123  
 Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser  
 330 335 340  
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 1171  
 Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val  
 345 350 355  
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 1219  
 Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly  
 360 365 370  
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 35 40 45  
 Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr  
 50 55 60  
 Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg  
 65 70 75 80  
 Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp  
 85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro  
 100 105 110  
 Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val  
 115 120 125  
 Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val  
 130 135 140  
 His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser  
 145 150 155 160  
 Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg  
 165 170 175  
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile  
 180 185 190  
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr  
 195 200 205  
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro  
 210 215 220  
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln  
 225 230 235 240  
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile  
 245 250 255  
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp  
 260 265 270  
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro  
 275 280 285  
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu  
 290 295 300  
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser  
 305 310 315 320  
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly  
 325 330 335  
 Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys  
 340 345 350  
 Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile  
 355 360 365  
 Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp  
 370 375 380  
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 Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly  
 405 410 415



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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA01692

<400> 817

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                                         Met Thr Ile Ser Gln
                                         1           5

gaa aac cag cca ata atc cag cca gtc tcc tta att ggt gga ggt cct 163
Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu Ile Gly Gly Gly Pro
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Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met Asn Arg Leu Gln Glu
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gct gat gtc att ttg gct gat cac ttg ggg ccc act gat gag ttg gaa 259
Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro Thr Asp Glu Leu Glu
                40                45                50

aaa ttg tgc gac atc agc tcg aag act gtt gtt gat gtg tcc aag ctt 307
Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val Asp Val Ser Lys Leu
                55                60                65

ccg tat ggg cgg cag gtc act cag gag cgt act aat gag atg ctt gtt 355
Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr Asn Glu Met Leu Val
                70                75                80                85

gaa tac gca cag cag gga cta aag gtg gtt cgc ctt aaa ggt ggt gac 403
Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg Leu Lys Gly Gly Asp
                90                95                100

cct tat gtc ttc ggt cgg ggt ttt gaa gag ttg gag ttt ttg ggc gag 451
Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu Glu Phe Leu Gly Glu
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cat gga att gaa tgc gag gtc att ccg ggt gtg acc agt gcg gtg tcc 499
His Gly Ile Glu Cys Glu Val Ile Pro Gly Val Thr Ser Ala Val Ser
                120                125                130

gtt cca gcg gcg gca ggt att cct att act aat ccg gga gtg gtg cat 547
Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn Arg Gly Val Val His
                135                140                145

tcc ttt acc gtg gtg tct gga cat ttg cct cca ggc cat ccg aag tca 595
Ser Phe Thr Val Val Ser Gly His Leu Pro Pro Gly His Pro Lys Ser
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Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly Gly Thr Leu Ser Ile
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 ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala Gln Ala Leu Met Asp  
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ggc ggg ctt gat gca gat act cca gca gct gtt att cag gaa ggc act 739  
 Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val Ile Gln Glu Gly Thr  
                   200                  205                  210

act gat gca caa cgc tca gtt cgg tgc acc ttg ggc aca ttg ggt gca 787  
 Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu Gly Thr Leu Gly Ala  
                   215                  220                  225

gtc atg gtg gag gaa gag att aag cct cca gct gtg tat gtc att gga 835  
 Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala Val Tyr Val Ile Gly  
                   230                  235                  240                  245

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 Gln Val Ala Gly Leu  
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<212> PRT

<213> Corynebacterium glutamicum

<400> 818

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Ile Gly Gly Gly Pro Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met  
                   20                  25                  30

Asn Arg Leu Gln Glu Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro  
                   35                  40                  45

Thr Asp Glu Leu Glu Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val  
                   50                  55                  60

Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr  
                   65                  70                  75                  80

Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg  
                   85                  90                  95

Leu Lys Gly Gly Asp Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu  
                   100                  105                  110

Glu Phe Leu Gly Glu His Gly Ile Glu Cys Glu Val Ile Pro Gly Val  
                   115                  120                  125

Thr Ser Ala Val Ser Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn  
                   130                  135                  140

Arg Gly Val Val His Ser Phe Thr Val Val Ser Gly His Leu Pro Pro  
                   145                  150                  155                  160

Gly His Pro Lys Ser Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly  
                   165                  170                  175

Gly Thr Leu Ser Ile Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala  
 180 185 190

Gln Ala Leu Met Asp Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val  
 195 200 205

Ile Gln Glu Gly Thr Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu  
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 <212> DNA  
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 <223> RXN00371

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aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163  
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser  
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gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211  
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val  
 25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259  
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro  
 40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307  
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu  
 55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355  
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr  
 70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403  
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile  
 90 95 100

cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451  
 Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg  
 105 110 115

atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt	499
Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg	
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Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly	
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Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr	
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Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val	
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Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile	
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Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu	
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Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala	
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cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat	883
Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn	
250 255 260	
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Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp	
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Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala Ala Ser Met Ser Ala	
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Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu Val Pro Thr Ile Ser  
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 Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala Ile Lys Gly  
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 Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser Val Asn Ala  
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 Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly Lys Pro His  
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 1917  
 Ser

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 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly  
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 85                                      90                                      95  
 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu  
 100                                      105                                      110  
 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg  
 115                                      120                                      125  
 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu  
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 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala  
 145                                      150                                      155                                      160  
 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu  
 165                                      170                                      175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly  
 180 185 190  
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro  
 195 200 205  
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val  
 210 215 220  
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro  
 225 230 235 240  
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu  
 245 250 255  
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala  
 260 265 270  
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu  
 275 280 285  
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu  
 290 295 300  
 Gly Lys Gly Val Asp Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg  
 305 310 315 320  
 Ala Leu Tyr Gly Trp Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala  
 325 330 335  
 Ala Ser Met Ser Ala Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu  
 340 345 350  
 Val Pro Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu  
 355 360 365  
 Arg Ala Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu  
 370 375 380  
 Thr Ser Val Asn Ala Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe  
 385 390 395 400  
 Gly Leu Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly  
 405 410 415  
 Glu Lys Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu  
 420 425 430  
 Leu Pro Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe  
 435 440 445  
 Pro Glu Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro  
 450 455 460  
 Arg Ala Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu  
 465 470 475 480  
 Gly Trp Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala  
 485 490 495

Pro Pro Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp  
                   500                                  505                                  510

Ala Val Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile  
                   515                                  520                                  525

Ala Gly Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met  
                   530                                  535                                  540

Thr Ala Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro  
 545                                  550                                  555                                  560

Glu Ile Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val  
                                   565                                  570                                  575

Ala Asp Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg  
                   580                                  585                                  590

Arg Arg Arg Lys Ala Ser  
                   595

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 <213> Corynebacterium glutamicum

<220>  
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 <223> FRXA00371

<400> 821

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acgttggtcg ttttcgagac aagtactaga aaagatatatg atg act atc gcc cat 115  
   Met Thr Ile Ala His  
   1                                  5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163  
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser  
                                   10                                  15                                  20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211  
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val  
                                   25                                  30                                  35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259  
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro  
                                   40                                  45                                  50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307  
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu  
                   55                                  60                                  65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355  
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr  
                   70                                  75                                  80                                  85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403  
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile



	90	95	100	
cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc				451
Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg				
	105	110	115	
atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt				499
Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg				
	120	125	130	
cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act				547
Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr				
	135	140	145	
cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga				595
Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly				
	150	155	160	165
gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca				643
Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr				
	170	175	180	
ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg				691
Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val				
	185	190	195	
gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att				739
Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile				
	200	205	210	
gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg				787
Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu				
	215	220	225	
gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc				835
Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala				
	230	235	240	245
cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat				883
Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn				
	250	255	260	
atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt				931
Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg				
	265	270	275	
ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat				979
Leu Gln Arg Thr Tyr Asp Thr Leu Leu Gly Leu Leu His Lys Leu Asp				
	280	285	290	
gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg				
1024				
Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val				
	295	300	305	

&lt;210&gt; 822

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 822

Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu  
 1 5 10 15  
 Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly  
 20 25 30  
 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr  
 35 40 45  
 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly  
 50 55 60  
 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala  
 65 70 75 80  
 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe  
 85 90 95  
 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu  
 100 105 110  
 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg  
 115 120 125  
 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu  
 130 135 140  
 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala  
 145 150 155 160  
 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu  
 165 170 175  
 Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly  
 180 185 190  
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro  
 195 200 205  
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val  
 210 215 220  
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro  
 225 230 235 240  
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu  
 245 250 255  
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala  
 260 265 270  
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu  
 275 280 285  
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu  
 290 295 300  
 Gly Lys Gly Val  
 305

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(732)  
 <223> FRXA00374

<400> 823  
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 Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala  
 1 5 10 15  
 atc aag ggc atc gtc gaa gga cgc tac cag tgg gtt gtc ctc aca agc 96  
 Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser  
 20 25 30  
 gtc aac gca gtg aag gca gtc tgg aag aaa atc acc gaa ttc ggc ctc 144  
 Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu  
 35 40 45  
 gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa 192  
 Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys  
 50 55 60  
 acc gcc gct gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct 240  
 Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro  
 65 70 75 80  
 gca cgt acc agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa 288  
 Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu  
 85 90 95  
 tat ttc gaa gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca 336  
 Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala  
 100 105 110  
 gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg 384  
 Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp  
 115 120 125  
 gaa gtc gaa gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca 432  
 Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro  
 130 135 140  
 agc gct gat atc cga gat atg atc aag acc ggc gga ttt gat gca gtt 480  
 Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val  
 145 150 155 160  
 gcc ttc acc tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt 528  
 Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly  
 165 170 175  
 aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca 576  
 Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala  
 180 185 190  
 gcg acc gct gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc 624

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile  
 195 200 205

gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat 672  
 Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp  
 210 215 220

ctg cgc gct aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt 720  
 Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg  
 225 230 235 240

cga aaa gcg tct taaaagggttt ttcactaggg tgt 755  
 Arg Lys Ala Ser

&lt;210&gt; 824

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 824

Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala  
 1 5 10 15

Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser  
 20 25 30

Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu  
 35 40 45

Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys  
 50 55 60

Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro  
 65 70 75 80

Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu  
 85 90 95

Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala  
 100 105 110

Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp  
 115 120 125

Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro  
 130 135 140

Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val  
 145 150 155 160

Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly  
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala  
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile  
 195 200 205

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp  
 210 215 220

Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg  
 225 230 235 240

Arg Lys Ala Ser

<210> 825  
 <211> 1467  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1444)  
 <223> RXN00383

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agccgtctcc atcattcatt cttaaactaa gaggagtttc atg cgt ttt gcc atc 115  
 Met Arg Phe Ala Ile  
 1 5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163  
 Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys  
 10 15 20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211  
 Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile  
 25 30 35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259  
 Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile  
 40 45 50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307  
 Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe  
 55 60 65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355  
 Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys  
 70 75 80 85

tct cag tat ttc gcg ggc ggt gcg ctg cat gcg ttc ccc gca ggt gga 403  
 Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala Phe Pro Ala Gly Gly  
 90 95 100

gtg atg ggt att cca agc aat cca cca gca ggc gcg caa gac acc gct 451  
 Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala  
 105 110 115

ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499  
 Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg  
 120 125 130

cgt cag tat ggc gat gag atc gtc gat act gtg gtg tct tcg ctg ctt 547  
 Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu

135	140	145	
ggt ggc gtt tat tcc tcc acc gct gat gat ctg ggt gtg cgc gct tcc Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu Gly Val Arg Ala Ser 150 155 160 165			595
gtg ccg gca ctt gct gca gcc ctt gat cag ctg gct gag gcc ggc gag Val Pro Ala Leu Ala Ala Leu Asp Gln Leu Ala Glu Ala Gly Glu 170 175 180			643
ccg gtg act ctg tca gct gcg gtc aag gcc gtg gaa gct cag cgg gaa Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val Glu Ala Gln Arg Glu 185 190 195			691
gcc gca aaa aca act tca gaa acc cgc ccc gtt ttc cag acc ttc aag Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val Phe Gln Thr Phe Lys 200 205 210			739
ggc gga tac gcg gag ctg tac gaa gcg ttg gca gag caa tgc ggt gca Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala Glu Gln Cys Gly Ala 215 220 225			787
gat att cac ttg gat agt ttc gtt tcc gcc atc acc aaa gat ggt gaa Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile Thr Lys Asp Gly Glu 230 235 240 245			835
ggt ttt gcc atc aag ggc ggt ggc gaa ggc acc tac gac aag gtg att Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr Tyr Asp Lys Val Ile 250 255 260			883
ttg gcg gtt ccc gct cca acc gcc gct gtg ctg ctc cgc gac ttg gca Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu Leu Arg Asp Leu Ala 265 270 275			931
ccg gcc gca gcg cca cat ttg cgc gca att aag ttg gct tct tca gca Pro Ala Ala Pro His Leu Arg Ala Ile Lys Leu Ala Ser Ser Ala 280 285 290			979
gtc gtc ggc atg cgt ttc gat tcc agc gag ggc ctg ccc gac aac tcc 1027 Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly Leu Pro Asp Asn Ser 295 300 305			
ggc gtc ctg gtc gct gtt aat gag ccg ggc atc acg gcg aag gcc ttc 1075 Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile Thr Ala Lys Ala Phe 310 315 320 325			
acg ttc tcc tca aag aag tgg cct cac ctg gag gct cgc ggg ggc gcg 1123 Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu Ala Arg Gly Gly Ala 330 335 340			
ctc gtg cgc gcg tcg ttc ggc agg cta ggc gat gag gcg tcg gca cgc 1171 Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp Glu Ala Ser Ala Arg 345 350 355			
atg gac gag gat ttg ctt gtc gac gcc gcc ctc gac gat ctc ctc acc 1219 Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu Asp Asp Leu Leu Thr			

360                      365                      370  
 ata acc ggg ttc gac ggc cgg gct gcc gga ctg ggt gaa att ttc gtg  
 1267  
 Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu Gly Glu Ile Phe Val  
 375                      380                      385  
 cag cgc tgg ttc ggt ggg ctc cca gcc tat gga gtt gat cac att gct  
 1315  
 Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly Val Asp His Ile Ala  
 390                      395                      400                      405  
 acc gtt tcg gct gcg cgt gca gag atc gca gcc gtg cct ggc gtg gaa  
 1363  
 Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala Val Pro Gly Val Glu  
 410                      415                      420  
 gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca  
 1411  
 Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val Pro Ala Val Ile Ala  
 425                      430                      435  
 gat gcc cag gca gca gta cac agg ttg ctg gga taagcaccca aaaacactat  
 1464  
 Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly  
 440                      445

tga  
1467

<210> 826  
 <211> 448  
 <212> PRT  
 <213> Corynebacterium glutamicum

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 Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu  
 20                      25                      30  
 Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser  
 35                      40                      45  
 Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp  
 50                      55                      60  
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser  
 65                      70                      75                      80  
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala  
 85                      90                      95  
 Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly  
 100                      105                      110  
 Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val  
 115                      120                      125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val  
 130 135 140  
 Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu  
 145 150 155 160  
 Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu  
 165 170 175  
 Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val  
 180 185 190  
 Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val  
 195 200 205  
 Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala  
 210 215 220  
 Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile  
 225 230 235 240  
 Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr  
 245 250 255  
 Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu  
 260 265 270  
 Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys  
 275 280 285  
 Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly  
 290 295 300  
 Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile  
 305 310 315 320  
 Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu  
 325 330 335  
 Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp  
 340 345 350  
 Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu  
 355 360 365  
 Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu  
 370 375 380  
 Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly  
 385 390 395 400  
 Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala  
 405 410 415  
 Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val  
 420 425 430  
 Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly  
 435 440 445



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<210> 827
<211> 382
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(382)
<223> FRXA00376
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agccgtctcc atcattcatt cttaaaactaa gaggagtttc atg cgt ttt gcc atc 115															
Met Arg Phe Ala Ile 5															
1															
atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163															
Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys 20															
10 15															
gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211															
Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile 35															
25 30															
ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259															
Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile 50															
40 45															
gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307															
Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe 65															
55 60															
act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355															
Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys 85															
70 75 80															
tct cag tat ttc gcg ggc ggt gcg ctg 382															
Ser Gln Tyr Phe Ala Gly Gly Ala Leu 90															
90															

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<210> 828
<211> 94
<212> PRT
<213> Corynebacterium glutamicum
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Met  Arg  Phe  Ala  Ile  Ile  Gly  Ala  Gly  Leu  Ala  Gly  Leu  Thr  Ala  Ala
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Tyr  Glu  Ile  His  Lys  Ala  Asp  Pro  Thr  Ala  Gln  Ile  Asp  Val  Leu  Glu
          20          25          30
Ala  Gly  Glu  Arg  Ile  Gly  Gly  Lys  Leu  Phe  Thr  Val  Pro  Phe  Ala  Ser
          35          40          45
Gly  Pro  Thr  Asp  Ile  Gly  Ala  Glu  Ala  Phe  Leu  Ala  Ala  Arg  Ser  Asp

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50	55	60
Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser		
65	70	75 80
Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu		
	85	90

<210> 829  
 <211> 1037  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1014)  
 <223> FRXA00383

<400> 829

gca ggc gcg caa gac acc gct ttt gat tgg act cct ggc caa gac att	48
Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile	
1 5 10 15	
tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat	96
Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp	
20 25 30	
act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat	144
Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp	
35 40 45	
gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat	192
Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Leu Asp	
50 55 60	
cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag	240
Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys	
65 70 75 80	
gcc gtg gaa gct cag cgg gaa gcc gca aaa aca act tca gaa acc cgc	288
Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg	
85 90 95	
ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg	336
Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala	
100 105 110	
ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc	384
Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser	
115 120 125	
gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt ggc gaa	432
Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu	
130 135 140	
ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct	480
Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala	
145 150 155 160	
gtg ctg ctc cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca	528

Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala  
 165 170 175

att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc 576  
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser  
 180 185 190

gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg 624  
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro  
 195 200 205

ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac 672  
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His  
 210 215 220

ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720  
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu  
 225 230 235 240

ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768  
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala  
 245 250 255

gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816  
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala  
 260 265 270

gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864  
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala  
 275 280 285

tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912  
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile  
 290 295 300

gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960  
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val  
 305 310 315 320

gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg  
 1008  
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu  
 325 330 335

ctg gga taagcaccca aaaacactat tga  
 1037  
 Leu Gly

&lt;210&gt; 830

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 830

Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile  
 1 5 10 15

Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp  
 20 25 30

Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp  
 35 40 45  
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp  
 50 55 60  
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys  
 65 70 75 80  
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg  
 85 90 95  
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala  
 100 105 110  
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser  
 115 120 125  
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu  
 130 135 140  
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala  
 145 150 155 160  
 Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala  
 165 170 175  
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser  
 180 185 190  
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro  
 195 200 205  
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His  
 210 215 220  
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu  
 225 230 235 240  
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala  
 245 250 255  
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala  
 260 265 270  
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala  
 275 280 285  
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile  
 290 295 300  
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val  
 305 310 315 320  
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu  
 325 330 335  
 Leu Gly

<210> 831  
 <211> 873  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(850)  
 <223> RXA01253

<400> 831  
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gagacctcaa aaaggctctg gagaaaggga ccgaacaata atg acc acc ctc aac 115  
 Met Thr Thr Leu Asn  
 1 5

atc ggc ctc atc ctc ccc gac gtc ctc gga act tac ggc gac gac ggc 163  
 Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr Tyr Gly Asp Asp Gly  
 10 15 20

aac gca cta gtc ctg cgc caa cgc gca cgc atg cgt ggc att aat gct 211  
 Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met Arg Gly Ile Asn Ala  
 25 30 35

gaa atc cag cgc gtc acc ctc gac gac gcc gtc cct tcc acc ctt gat 259  
 Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val Pro Ser Thr Leu Asp  
 40 45 50

ctc tac tgc ctc ggc ggc ggc gag gac acc gca cag atc ctt gcc acc 307  
 Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala Gln Ile Leu Ala Thr  
 55 60 65

gaa cac ctc acc aaa gac ggc ggc ctc caa acc gca gcc gcc gca ggc 355  
 Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr Ala Ala Ala Ala Gly  
 70 75 80 85

cgc ccc atc ttc gca gtc tgc gca ggt ctc cag gta ctc ggc gac tcc 403  
 Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln Val Leu Gly Asp Ser  
 90 95 100

ttc cgc gcc gcc ggc cgt gtc atc gac ggc ctt ggg ctt atc gac gcc 451  
 Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu Gly Leu Ile Asp Ala  
 105 110 115

acc acc gtc tct tta caa aaa cgc gcc atc gga gaa gtc gaa acg aca 499  
 Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly Glu Val Glu Thr Thr  
 120 125 130

cca acc cgc gcc gga ttc acc gcc gag ctg acc gaa cga ctc acc ggc 547  
 Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr Glu Arg Leu Thr Gly  
 135 140 145

ttc gaa aac cac atg ggc gcc acc ctg ctc ggc ccc gac gcc gaa cca 595  
 Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly Pro Asp Ala Glu Pro  
 150 155 160 165

ctc ggc cga gtc gtc cgc ggc gaa ggc aac acc gat gtc tgg gca gcc 643  
 Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr Asp Val Trp Ala Ala  
 170 175 180

tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc 691  
 Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val  
                   185                  190                  195

caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga 739  
 Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg  
                   200                  205                  210

aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg 787  
 Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala  
                   215                  220                  225

ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc 835  
 Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg  
                   230                  235                  240                  245

gcc gaa cgc ctg gcg tagcccccttc taaaccgggt cta 873  
 Ala Glu Arg Leu Ala  
                   250

&lt;210&gt; 832

&lt;211&gt; 250

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 832

Met Thr Thr Leu Asn Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr  
   1                  5                  10                  15

Tyr Gly Asp Asp Gly Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met  
                   20                  25                  30

Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val  
                   35                  40                  45

Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala  
                   50                  55                  60

Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr  
                   65                  70                  75                  80

Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln  
                   85                  90                  95

Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu  
                   100                  105                  110

Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly  
                   115                  120                  125

Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr  
                   130                  135                  140

Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly  
                   145                  150                  155                  160

Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr  
                   165                  170                  175

Asp Val Trp Ala Ala Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe  
 180 185 190

Ala Glu Gly Ala Val Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly  
 195 200 205

Pro Ala Leu Ala Arg Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys  
 210 215 220

Ala Met Gly Val Ala Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val  
 225 230 235 240

Ile Asp Arg Leu Arg Ala Glu Arg Leu Ala  
 245 250

&lt;210&gt; 833

&lt;211&gt; 1044

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1021)

&lt;223&gt; RXA02134

&lt;400&gt; 833

tgatgaacga catgtcgaca ttttcttccg ccggcgctcga tggacccta aacgcctctt 60

ccgaagcgcc cgagcaaaac acggagtaac tttctaagcg atg tcc ggc aaa gca 115  
 Met Ser Gly Lys Ala  
 1 5

ggc ttt acc ccc gaa gat ccc gaa gac tca gac aac cgc cac ggg aac 163  
 Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp Asn Arg His Gly Asn  
 10 15 20

ccc ctt ttc gaa ggt atc ttt acc gca ctt aat tgg atg acc gtt ctc 211  
 Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn Trp Met Thr Val Leu  
 25 30 35

ccc gtc ccc ggc gca tca gtt ttt gat cgc acc acg ggc gcc cgg gta 259  
 Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr Thr Gly Ala Arg Val  
 40 45 50

atg gcc tct ttg ccc ttt gtt ggc ttc gtt ttc gga atg ttc acc gcg 307  
 Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe Gly Met Phe Thr Ala  
 55 60 65

atc atc atg tgg gct atc ggc ccc att tca ggg gtg atc cac gtc gat 355  
 Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly Val Ile His Val Asp  
 70 75 80 85

gga ctt tta gtt gcc gtt ctg atc gtc gcg ttc tgg gaa ctt ctt aat 403  
 Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe Trp Glu Leu Leu Asn  
 90 95 100

cgg ttt atg cac ctc gac ggc ctc gca gat gtc tcc gat gct ttg ggt 451  
 Arg Phe Met His Leu Asp Gly Leu Ala Asp Val Ser Asp Ala Leu Gly  
 105 110 115

tcc tac gca gcc cca cca cgc gca cga gaa atc ctt gcc gat ccc cgc 499  
 Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile Leu Ala Asp Pro Arg  
 120 125 130

acc gga ctt ttc ggc ctc gcc acc gcc atg ctt tcc gtt ctc ctg cag 547  
 Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu Ser Val Leu Leu Gln  
 135 140 145

gtc gct gca gtc gca tcg ctt gtc gat tca acc gtg tgg tgg atg atc 595  
 Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr Val Trp Trp Met Ile  
 150 155 160 165

tgc ttc atc ccc gtt ctc ggc cgc atc gct gga caa gta acc gca ctg 643  
 Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly Gln Val Thr Ala Leu  
 170 175 180

aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691  
 Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile  
 185 190 195

gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739  
 Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala  
 200 205 210

gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787  
 Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu  
 215 220 225

acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835  
 Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile  
 230 235 240 245

aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883  
 Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala  
 250 255 260

tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931  
 Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly  
 265 270 275

gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979  
 Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser  
 280 285 290

att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg  
 1021  
 Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val  
 295 300 305

taaagcgggtg gcgtcttttg gga  
 1044

&lt;210&gt; 834

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 834

Met Ser Gly Lys Ala Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp  
 1 5 10 15



Asn Arg His Gly Asn Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn  
 20 25 30  
 Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr  
 35 40 45  
 Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe  
 50 55 60  
 Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly  
 65 70 75 80  
 Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe  
 85 90 95  
 Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val  
 100 105 110  
 Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile  
 115 120 125  
 Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu  
 130 135 140  
 Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr  
 145 150 155 160  
 Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly  
 165 170 175  
 Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe  
 180 185 190  
 Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp  
 195 200 205  
 Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser  
 210 215 220  
 Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro  
 225 230 235 240  
 Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile  
 245 250 255  
 Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu  
 260 265 270  
 Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile  
 275 280 285  
 His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn  
 290 295 300  
 Ala Met Val  
 305

&lt;210&gt; 835

&lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1174)

&lt;223&gt; RXA02135

&lt;400&gt; 835

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cgtgtcgcag cgatttgcga gaggggttgtc ttcgtgggttg ctggtctgcc actagagttg 60
aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag 115
                                         Met Val Pro Ala Glu
                                         1           5

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
                10                15                20

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211
Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys
                25                30                35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg 259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro
                40                45                50

cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac 307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His
                55                60                65

ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg 355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu
                70                75                80                85

cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att 403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile
                90                95                100

gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac 451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp
                105                110                115

cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc 499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile
                120                125                130

gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag 547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys
                135                140                145

atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att 595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile
                150                155                160                165

tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc 643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala
                170                175                180

ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc 691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg

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185	190	195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile 200 205 210			739
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala 215 220 225			787
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe 230 235 240 245			835
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val 250 255 260			883
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala 265 270 275			931
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser 280 285 290			979
gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg 1027 Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met 295 300 305			
tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag 1075 Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys 310 315 320 325			
att gcc gtt gac ctg atg aac gac atg tgc aca ttt tct tcc gcc ggc 1123 Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly 330 335 340			
gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg 1171 Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr 345 350 355			
gag taactttcta agcgatgtcc ggc 1197 Glu			

&lt;210&gt; 836

&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 836

Met	Val	Pro	Ala	Glu	Leu	Phe	Ala	Arg	Val	Glu	Phe	Pro	Asp	His	Lys
1					5					10					15

Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro  
 20 25 30  
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys  
 35 40 45  
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val  
 50 55 60  
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro  
 65 70 75 80  
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala  
 85 90 95  
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile  
 100 105 110  
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg  
 115 120 125  
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val  
 130 135 140  
 Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp  
 145 150 155 160  
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr  
 165 170 175  
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val  
 180 185 190  
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu  
 195 200 205  
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg  
 210 215 220  
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala  
 225 230 235 240  
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val  
 245 250 255  
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys  
 260 265 270  
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr  
 275 280 285  
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile  
 290 295 300  
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala  
 305 310 315 320  
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr  
 325 330 335  
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala

340 345 350

Pro Glu Gln Asn Thr Glu  
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<210> 837  
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<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (101)..(622)  
<223> RXA02136

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Met Arg Thr Leu Val  
1 5

ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163  
Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val  
10 15 20

gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211  
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp  
25 30 35

gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259  
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro  
40 45 50

acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307  
Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val Asp Lys Leu Leu Ala  
55 60 65

tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355  
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu  
70 75 80 85

acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403  
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln  
90 95 100

ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451  
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln  
105 110 115

ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499  
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val  
120 125 130

ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat cgc atc ggc aca ctt 547  
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu  
135 140 145

aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595  
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala

150                      155                      160                      165

ggt ctg cca cta gag ttg aaa acg ttt taagaaaaca gtcggtttga          642  
Gly Leu Pro Leu Glu Leu Lys Thr Phe

170

agg 645

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<210> 838
<211> 174
<212> PRT
<213> Corynebacterium glutamicum
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20 25 30

Arg Pro Ser Gly Asp Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His  
35 40 45

Ala Glu Arg Arg Pro Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val  
50 55 60

Asp Lys Leu Leu Ala Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp  
65 70 75 80

Leu Gly Thr Trp Leu Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu  
85 90 95

Ala Ser Ser Ala Gln Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala  
100 105 110

Ile Leu His Phe Gln Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val  
115 120 125

Gly Met Gly Ile Val Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp  
130 135 140

Arg Ile Gly Thr Leu Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val  
145 150 155 160

Val Phe Val Val Ala Gly Leu Pro Leu Glu Leu Lys Thr Phe  
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<213> Corynebacterium glutamicum
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<222> (1)..(552)  
<223> RXN03114
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 cgc cgc gag ttg acg gtg ggg ttg gat gct ggt gac ggt ccg att tta 96  
 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu  
 20 25 30  
 agg cag agc ttt gat gtt ggt ttt ttg ctt gtc gac gcc tcc ttc cac 144  
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His  
 35 40 45  
 att cat atc aat ggc gtg tct act ggg cag tcg gtt gcg ccg gat gat 192  
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp  
 50 55 60  
 gta gtt gag gtg gtg cgt ggt ttg gct gat gct tcg gag ttg tcc gtg 240  
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val  
 65 70 75 80  
 gaa agt gtt gct gag ttg tgt act ccc gtg gca ccg gtt tca tta tct 288  
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser  
 85 90 95  
 gag gca cag ggg aat cct gcg cct att ggg tgg ttg gag cat gat ggc 336  
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly  
 100 105 110  
 gtg gtg tcg ttg ggt gcg ggt att cca ggg ggg cgg gtg gag gct cgt 384  
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg  
 115 120 125  
 tta gcg cgt ttt att gcg gtg att gag gcg gag acc act att acc cca 432  
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro  
 130 135 140  
 tgg aat tcg ttg atc att cat gat ttg tat gag ggt gtt gca gaa cag 480  
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln  
 145 150 155 160  
 gtg gtg aag gtt ctg gct ccc atg ggg ttg gtt ttt gat gct aat tca 528  
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser  
 165 170 175  
 ccg ctt ctg gag tca ccg gct ttg taactcgcca ttggtgcacg tct 575  
 Pro Leu Leu Glu Ser Pro Ala Leu  
 180

&lt;210&gt; 840

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 840

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val  
 1 5 10 15

Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu  
 20 25 30

Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His

[illegible]

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<210> 841
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1177)
<223> RXN01810
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gcttcaccgt																	cggcaacccg	actggaaaat	aaggcttcac	atg	aat	aac	gct	ttt	115	
										Met	Asn	Asn	Ala	Phe												
										1					5											
cga	cgc	acc	ctt	aca	tcc	gta	gtc	ctc	gcc	gct	agc	ttg	gcc	tta	acg	163										
Arg	Arg	Thr	Leu	Thr	Ser	Val	Val	Leu	Ala	Ala	Ser	Leu	Ala	Leu	Thr											
				10					15					20												
gcc	tgc	gca	agc	tgg	gat	tca	cct	acg	gca	tct	tcc	aat	ggg	gat	ctg	211										
Ala	Cys	Ala	Ser	Trp	Asp	Ser	Pro	Thr	Ala	Ser	Ser	Asn	Gly	Asp	Leu											
			25					30					35													
att	gag	gag	atc	cag	gca	agc	tcc	acc	tca	aca	gat	ccg	cgc	acc	ttc	259										
Ile	Glu	Glu	Ile	Gln	Ala	Ser	Ser	Thr	Ser	Thr	Asp	Pro	Arg	Thr	Phe											
			40					45					50													
aca	ggc	ttg	agc	atc	gtg	gaa	gat	atc	ggc	gat	gtg	gtt	ccc	gta	acc	307										
Thr	Gly	Leu	Ser	Ile	Val	Glu	Asp	Ile	Gly	Asp	Val	Val	Pro	Val	Thr											



55	60	65	
gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly 70 75 80 85			355
aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu 90 95 100			403
tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn 105 110 115			451
att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile 120 125 130			499
gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt Glu Val Val Thr Thr Gly Gly His Thr Leu Asn Ala Glu Ala Ile Leu 135 140 145			547
aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg 150 155 160 165			595
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met 170 175 180			643
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile 185 190 195			691
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg 200 205 210			739
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr 215 220 225			787
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly 230 235 240 245			835
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile 250 255 260			883
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp 265 270 275			931
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val 280 285 290			979
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt 1027 Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly			

295                      300                      305  
 ctt atg gaa cgc ccc ggc att gct cag aca acc gcc gga caa aac caa  
 1075  
 Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr Ala Gly Gln Asn Gln  
 310                      315                      320                      325  
 cga gta ctg gcg ctt ccc gat ggt caa tca ttg gcc ttt ggt gcc caa  
 1123  
 Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu Ala Phe Gly Ala Gln  
 330                      335                      340  
 act ggc gag ttg ttg ctc cgc gca tcc cgc gaa ctg tat gtg cag ggc  
 1171  
 Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu Leu Tyr Val Gln Gly  
 345                      350                      355  
 ggc gag tagatggttg tgaaggaggt tga  
 1200  
 Gly Glu

<210> 842  
 <211> 359  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 842  
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 Ser Leu Ala Leu Thr Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser  
 20                      25                      30  
 Ser Asn Gly Asp Leu Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr  
 35                      40                      45  
 Asp Pro Arg Thr Phe Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp  
 50                      55                      60  
 Val Val Pro Val Thr Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu  
 65                      70                      75                      80  
 Thr Asp Ala Asp Gly Asn Asp Val Val Val Glu Asn Val Ser Arg Ile  
 85                      90                      95  
 Leu Pro Leu Asp Leu Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu  
 100                      105                      110  
 Gly Leu Val Asp Asn Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro  
 115                      120                      125  
 Ala Leu Ala Asp Ile Glu Val Val Thr Thr Gly Gly His Thr Leu Asn  
 130                      135                      140  
 Ala Glu Ala Ile Leu Asn Leu His Pro Thr Leu Val Ile Ile Asp His  
 145                      150                      155                      160  
 Ser Ile Gly Pro Arg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val  
 165                      170                      175

Ala Thr Val Ile Met Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp  
 180 185 190

Asp Ile Arg Asp Ile Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu  
 195 200 205

Lys Leu Ala Glu Arg Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val  
 210 215 220

Val Asp Glu Leu Thr Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr  
 225 230 235 240

Ala Arg Gly Thr Gly Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly  
 245 250 255

Gly Arg Asp Leu Ile Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu  
 260 265 270

Lys Gly Ile Met Asp Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu  
 275 280 285

Leu Asn Pro Asp Val Phe Val Met Met Ser Glu Gly Leu Val Ser Thr  
 290 295 300

Gly Gly Ile Asp Gly Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr  
 305 310 315 320

Ala Gly Gln Asn Gln Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu  
 325 330 335

Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu  
 340 345 350

Leu Tyr Val Gln Gly Gly Glu  
 355

&lt;210&gt; 843

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (933)

&lt;223&gt; RXS03205

&lt;400&gt; 843

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Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro	
1 5 10 15	
gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln	
165 170 175	
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc	576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg	
180 185 190	
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc	624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg	
195 200 205	
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat	672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp	
210 215 220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc	720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg	
225 230 235 240	
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc	768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser	
245 250 255	
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg	816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu	
260 265 270	
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac	864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn	
275 280 285	
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg	912

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu  
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccgtttt 963  
 Pro Ala Asp Leu Leu Asp Ser  
 305 310

<210> 844

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 844

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu  
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala  
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly  
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr  
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu  
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys  
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu  
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln  
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg  
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg  
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp  
 210 215 220

Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg  
 225 230 235 240

Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser  
 245 250 255

Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu  
260 265 270

Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn  
275 280 285

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu  
290 295 300

Pro Ala Asp Leu Leu Asp Ser  
305 310

<210> 845

<211> 956

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(933)

<223> FRXA00306

<400> 845

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1 5 10 15	
gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	
cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	

gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa 480  
 Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu  
 145 150 155 160  
 gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag 528  
 Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln  
 165 170 175  
 tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576  
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg  
 180 185 190  
 acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624  
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg  
 195 200 205  
 ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672  
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp  
 210 215 220  
 gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720  
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg  
 225 230 235 240  
 acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768  
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser  
 245 250 255  
 atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816  
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu  
 260 265 270  
 gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864  
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn  
 275 280 285  
 ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912  
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu  
 290 295 300  
 ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956  
 Pro Ala Asp Leu Leu Asp Ser  
 305 310

&lt;210&gt; 846

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 846

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
 1 5 10 15  
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30  
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45  
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu

50	55	60
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala 65 70 75 80		
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly 85 90 95		
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr 100 105 110		
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu 115 120 125		
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys 130 135 140		
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu 145 150 155 160		
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln 165 170 175		
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg 180 185 190		
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg 195 200 205		
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp 210 215 220		
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg 225 230 235 240		
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser 245 250 255		
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu 260 265 270		
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn 275 280 285		
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu 290 295 300		
Pro Ala Asp Leu Leu Asp Ser 305 310		

&lt;210&gt; 847

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (796)

&lt;223&gt; RXC01715





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 Val Leu Pro  
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 <212> PRT  
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 Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg  
                     20                      25                      30  
 Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala  
                     35                      40                      45  
 Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg  
                     50                      55                      60  
 Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp  
                     65                      70                      75                      80  
 Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln  
                     85                      90                      95  
 Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu  
                     100                      105                      110  
 Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys  
                     115                      120                      125  
 Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile  
                     130                      135                      140  
 Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala  
                     145                      150                      155                      160  
 Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala  
                     165                      170                      175  
 Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His  
                     180                      185                      190  
 Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu  
                     195                      200                      205  
 His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile  
                     210                      215                      220  
 Ala Asp Leu Ile Lys Val Leu Pro  
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&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1564)

&lt;223&gt; RXN00420

&lt;400&gt; 849

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ttcaccacct gaaaattttc gggggtaacc tttaaaggcg atg aac agt tct cac 115
                                         Met Asn Ser Ser His
                                         1           5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
              10              15              20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
              25              30              35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
              40              45              50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
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ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
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aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
              90              95              100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
              105              110              115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
              120              125              130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
              135              140              145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
              150              155              160              165

gtg gtc tcc atg gaa ctc ctc gtt gca gac gga cgc atc ctg cac ctc 643
Val Val Ser Met Glu Leu Leu Val Ala Asp Gly Arg Ile Leu His Leu
              170              175              180

gag cca gaa ggc acc gcc gaa gac cca cag ggc gac ctg ttc tgg gca 691
Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly Asp Leu Phe Trp Ala

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185	190	195	
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cgc atg acc aag acg gaa acc gcc tac ttc att gcg gac acc gac cgc Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg 215 220 225			787
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu 230 235 240 245			835
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu 250 255 260			883
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu 265 270 275			931
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys 280 285 290			979
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atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc tac 1123 Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr 330 335 340			
caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag 1171 Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys 345 350 355			
ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct 1219 Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro 360 365 370			
ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca 1267 Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala 375 380 385			
ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc 1315 Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser 390 395 400 405			

tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc cca  
 1363  
 Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro  
 410 415 420

ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc  
 1411  
 Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe  
 425 430 435

ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac  
 1459  
 Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn  
 440 445 450

ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat  
 1507  
 Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn  
 455 460 465

gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt  
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 Glu Leu Ser

<210> 850  
 <211> 488  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 850  
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 20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile  
 35 40 45

Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro  
 50 55 60

Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr  
 65 70 75 80

Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro  
 85 90 95

Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val  
 100 105 110

Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr  
 115 120 125

Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly  
 130 135 140  
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly  
 145 150 155 160  
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly  
 165 170 175  
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly  
 180 185 190  
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile  
 195 200 205  
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile  
 210 215 220  
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His  
 225 230 235 240  
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp  
 245 250 255  
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly  
 260 265 270  
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala  
 275 280 285  
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp  
 290 295 300  
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly  
 305 310 315 320  
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn  
 325 330 335  
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg  
 340 345 350  
 Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr  
 355 360 365  
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser  
 370 375 380  
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn  
 385 390 395 400  
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp  
 405 410 415  
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys  
 420 425 430  
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg  
 435 440 445  
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp

450                      455                      460  
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 465                      470                      475                      480  
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 <213> Corynebacterium glutamicum  
  
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 <223> FRXA00420  
  
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 gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc 96  
 Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe  
 20                      25                      30  
 tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc 144  
 Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser  
 35                      40                      45  
 aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag 192  
 Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu  
 50                      55                      60  
 cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc 240  
 Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser  
 65                      70                      75                      80  
 gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg 288  
 Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu  
 85                      90                      95  
 tcc tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc 336  
 Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg  
 100                      105                      110  
 cca ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa 384  
 Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu  
 115                      120                      125  
 ttc ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag 432  
 Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu  
 130                      135                      140  
 aac ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga 480  
 Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg  
 145                      150                      155                      160  
 aat gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga 528

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg  
 165 170 175

ctt gag ctt tct taagaaaggg cttgaactaa aca  
 Leu Glu Leu Ser  
 180

563

&lt;210&gt; 852

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 852

Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr  
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Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe  
 20 25 30

Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser  
 35 40 45

Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu  
 50 55 60

Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser  
 65 70 75 80

Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu  
 85 90 95

Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg  
 100 105 110

Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu  
 115 120 125

Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu  
 130 135 140

Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg  
 145 150 155 160

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg  
 165 170 175

Leu Glu Leu Ser  
 180

&lt;210&gt; 853

&lt;211&gt; 622

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(622)

&lt;223&gt; FRXA00426



&lt;400&gt; 853

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Met Asn Ser Ser His  
1 5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163  
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro  
10 15 20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211  
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr  
25 30 35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259  
Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val  
40 45 50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307  
Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg  
55 60 65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355  
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln  
70 75 80 85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403  
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His  
90 95 100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451  
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr  
105 110 115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499  
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro  
120 125 130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547  
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro  
135 140 145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595  
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His  
150 155 160 165

gtg gtc tcc atg gaa ctc ctc gtt gca 622  
Val Val Ser Met Glu Leu Leu Val Ala  
170

&lt;210&gt; 854

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 854

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1 5 10 15

His	Gly	Ala	Leu	Pro	Leu	Glu	Ala	Gln	Lys	Leu	Asn	Gly	Trp	Gly	Arg
			20					25					30		
Thr	Ala	Pro	Thr	Thr	Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile
		35					40					45			
Ile	Val	Asp	Ala	Val	Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro
	50					55					60				
Asp	Tyr	Leu	Lys	Arg	Gly	Val	Ile	Ala	Arg	Gly	Met	Gly	Arg	Ser	Tyr
65					70					75					80
Gly	Asp	Pro	Ala	Gln	Asn	Ala	Gly	Gly	Leu	Val	Ile	Asp	Met	Gln	Pro
				85					90					95	
Leu	Asn	Lys	Ile	His	Ser	Ile	Asp	Pro	Asp	Ser	Ala	Ile	Val	Asp	Val
			100					105					110		
Asp	Gly	Gly	Val	Thr	Leu	Asp	Gln	Leu	Met	Lys	Ala	Ala	Leu	Pro	Tyr
		115					120					125			
Gly	Leu	Trp	Val	Pro	Val	Leu	Pro	Gly	Thr	Arg	Gln	Val	Thr	Ile	Gly
	130					135					140				
Gly	Ala	Ile	Gly	Pro	Asp	Ile	His	Gly	Lys	Asn	His	His	Ser	Ala	Gly
145					150					155					160
Ser	Phe	Gly	Asp	His	Val	Val	Ser	Met	Glu	Leu	Leu	Val	Ala		
				165					170						

<210> 855

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$ 

<221> CDS

<222> (101) .. (907)

<223> RXN00708

<400> 855

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Met Thr Leu Ser Leu  
1 5

cct cca att ggt ttc ggc acc gtt cat ctt gat ggc gca cct ggc gtt 163  
Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp Gly Ala Pro Gly Val  
10 15 20

gaa gcc atc gct act gcc att gat gct ggt tac cgc ctc atc gac acc 211  
Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr Arg Leu Ile Asp Thr  
25 30 35

gcg tac aac tat gaa aat gaa ggt acc gtg ggc aag gct gtc cgc gag 259  
Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly Lys Ala Val Arg Glu  
40 45 50

tcg ggt gtc ccc cgc gag gaa ttg att gtt acc agt aag ctc cct ggc 307

Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly		
55						60					65						
cgc	ttc	cat	gct	cgc	gat	cta	gga	cgc	gtc	cgc	att	gag	gaa	agt	cta	355	
Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	85	
70					75				80								
tac	cgc	ctc	aac	tta	gat	tac	atc	gat	ctc	ctc	ttg	att	cac	tgg	cct	403	
Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	100	
				90					95								
aat	ccc	agc	aag	gat	ctc	tac	gtc	gag	gcg	tgg	gaa	acg	ctg	att	gaa	451	
Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	115	
			105					110									
gtc	cgc	gat	gct	ggc	ctg	gtc	aag	cac	atc	gga	gtg	tct	aac	ttc	ctt	499	
Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	His	Ile	Gly	Val	Ser	Asn	Phe	Leu		
			120				125					130					
cca	aat	cac	att	gat	cgc	ctg	cgc	cgc	gaa	acc	ggt	gaa	ctg	ccg	gcc	547	
Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala		
			135			140					145						
gtt	aac	cag	atc	gag	ttg	cac	ccc	tat	ttc	ccg	cag	gtg	gag	cag	gta	595	
Val	Asn	Gln	Ile	Glu	Leu	His	Pro	Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val		
150					155				160						165		
gat	ttc	cac	gat	gag	ctg	ggc	atc	att	acc	gag	gcc	tgg	agc	ccg	ctc	643	
Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu		
				170					175					180			
agc	aac	ggt	cgc	gga	ctc	gtc	gaa	gag	cca	ttg	ctc	aag	gaa	atc	ggc	691	
Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly		
			185					190					195				
gag	cgc	tac	ggg	gtc	ggc	agc	ggc	gaa	atc	gcc	ctc	gct	tgg	cat	cac	739	
Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	Glu	Ile	Ala	Leu	Ala	Trp	His	His		
			200				205					210					
gcc	agg	gga	atc	gtt	ccg	att	cca	cgc	tcc	acc	aac	ccg	gcc	agg	cag	787	
Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln		
			215			220					225						
cgc	agc	aac	ttg	gag	gcg	gta	aag	att	tcg	ctt	atc	gac	gaa	gac	gtc	835	
Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val		
230					235					240					245		
cag	gcg	att	acc	gct	ttg	gcg	cgc	aaa	aac	ggc	cgg	atc	aaa	gat	caa	883	
Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln		
				250				255						260			
gat	cca	gcc	gtc	tat	gaa	gaa	ttc	tagatagtt	catcaagg	ggt	ccg					930	
Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe										
				265													

&lt;210&gt; 856

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 856

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Met Thr Leu Ser Leu Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp
 1           5           10           15

Gly Ala Pro Gly Val Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr
          20           25           30

Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly
          35           40           45

Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr
          50           55           60

Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg
          65           70           75           80

Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu
          85           90           95

Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp
          100          105          110

Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly
          115          120          125

Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr
          130          135          140

Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro
          145          150          155          160

Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu
          165          170          175

Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu
          180          185          190

Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala
          195          200          205

Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr
          210          215          220

Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu
          225          230          235          240

Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly
          245          250          255

Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
          260          265

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&lt;210&gt; 857

&lt;211&gt; 695

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(672)

&lt;223&gt; FRXA00708

&lt;400&gt; 857

acc	gtg	ggc	aag	gct	gtc	cgc	gag	tcg	ggg	gtc	ccc	cgc	gag	gaa	ttg	48
Thr	Val	Gly	Lys	Ala	Val	Arg	Glu	Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	
1				5					10					15		
att	gtt	acc	agt	aag	ctc	cct	ggc	cgc	ttc	cat	gct	cgc	gat	cta	gga	96
Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly	Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	
			20					25					30			
cgc	gtc	cgc	att	gag	gaa	agt	cta	tac	cgc	ctc	aac	tta	gat	tac	atc	144
Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	
		35					40					45				
gat	ctc	ctc	ttg	att	cac	tgg	cct	aat	ccc	agc	aag	gat	ctc	tac	gtc	192
Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	
	50					55					60					
gag	gcg	tgg	gaa	acg	ctg	att	gaa	gtc	cgc	gat	gct	ggc	ctg	gtc	aag	240
Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	
65					70				75						80	
cac	atc	gga	gtg	tct	aac	ttc	ctt	cca	aat	cac	att	gat	cgc	ctg	cgc	288
His	Ile	Gly	Val	Ser	Asn	Phe	Leu	Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	
				85					90					95		
cgc	gaa	acc	ggg	gaa	ctg	ccg	gcc	gtt	aac	cag	atc	gag	ttg	cac	ccc	336
Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala	Val	Asn	Gln	Ile	Glu	Leu	His	Pro	
			100					105					110			
tat	ttc	ccg	cag	gtg	gag	cag	gta	gat	ttc	cac	gat	gag	ctg	ggc	atc	384
Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val	Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	
		115					120					125				
att	acc	gag	gcc	tgg	agc	ccg	ctc	agc	aac	ggg	cgc	gga	ctc	gtc	gaa	432
Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu	Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	
	130					135					140					
gag	cca	ttg	ctc	aag	gaa	atc	ggc	gag	cgc	tac	ggg	gtc	ggc	agc	ggc	480
Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly	Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	
145					150				155						160	
gaa	atc	gcc	ctc	gct	tgg	cat	cac	gcc	agg	gga	atc	gtt	ccg	att	cca	528
Glu	Ile	Ala	Leu	Ala	Trp	His	His	Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	
				165				170					175			
cgc	tcc	acc	aac	ccg	gcc	agg	cag	cgc	agc	aac	ttg	gag	gcg	gta	aag	576
Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln	Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	
			180					185					190			
att	tcg	ctt	atc	gac	gaa	gac	gtc	cag	gcg	att	acc	gct	ttg	gcg	cgc	624
Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val	Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	
		195					200					205				
aaa	aac	ggc	cgg	atc	aaa	gat	caa	gat	cca	gcc	gtc	tat	gaa	gaa	ttc	672
Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln	Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe	
	210					215					220					
tagatagttta	catcaagggtt	ccg														695

&lt;210&gt; 858

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 858

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Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu
  1              5              10              15

Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly
          20              25              30

Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile
          35              40              45

Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
  50              55              60

Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
  65              70              75              80

His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
          85              90              95

Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
          100              105              110

Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
          115              120              125

Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
          130              135              140

Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly
          145              150              155              160

Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
          165              170              175

Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
          180              185              190

Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg
          195              200              205

Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
          210              215              220

```

&lt;210&gt; 859

&lt;211&gt; 1038

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1015)

&lt;223&gt; RXA02373

&lt;400&gt; 859

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aaagtcataag ctcatggttaa ttcagtgtag ataggcgtac ggtgggctat ccaattcatc 60

tcaacctaag gcgcattttg gtgcgcatca aggagaaaat atg tct gtt gtg ggt 115
                                   Met Ser Val Val Gly
                                   1       5

acc ggc cta ttc ttt gga tcc ccg gag gaa gag cgg gat aag ttg atg 163
Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu Arg Asp Lys Leu Met
              10              15              20

caa tct ttg atg gat cag aag aat aag ctt tcg aag tct gaa ggt atc 211
Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser Lys Ser Glu Gly Ile
              25              30              35

cca ttg gtc acc ttg aat gat gga aaa acc att cct cag ctt ggt ttt 259
Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile Pro Gln Leu Gly Phe
              40              45              50

ggt gtg ttc aag gta gat ccc gat gaa gca gag cgc gta gtt acc gaa 307
Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu Arg Val Val Thr Glu
              55              60              65

gca ctt gag gta ggt tac cgc cac atc gat act gct gcg att tac ggc 355
Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala Ile Tyr Gly
              70              75              80              85

aat gag gaa ggt gtc ggc cga gct att gct aag tcc ggc att cct cgt 403
Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys Ser Gly Ile Pro Arg
              90              95              100

gaa gag ctg ttt att act acc aag ttg tgg aac gat cgc cac ctg gat 451
Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg His Leu Asp
              105              110              115

gta gaa gct gct ttt gag gag tct ctg cag aag ctg ggc ttg gat tat 499
Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys Leu Gly Leu Asp Tyr
              120              125              130

gta gat ctg tac ttg gtg cac tgg ccg gca ccg aag aac gat aat tat 547
Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro Lys Asn Asp Asn Tyr
              135              140              145

gtt gct gca tgg aag ggc ttg gaa aag ctc ggt gac cgt gct cgt tcc 595
Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly Asp Arg Ala Arg Ser
              150              155              160              165

atc ggt gtg tgc aac ttc ctg cca gag cac cta gaa aag ctg ctg gca 643
Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu Glu Lys Leu Leu Ala
              170              175              180

gag gca acc act gtg cct gcc att aac cag att gag ctg cac cca gct 691
Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile Glu Leu His Pro Ala
              185              190              195

ttg cag cag cgc gat gct gtt gag gca tct ctt gca gca ggc atc act 739
Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu Ala Ala Gly Ile Thr
              200              205              210

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gtg gag tcg tgg ggt cct ctg gga cag ggg cgt ttt gat ctt ggc gct 787  
 Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg Phe Asp Leu Gly Ala  
 215 220 225  
  
 gag gaa cca atc gca gct gca gcg aag aac cat gga aag acc cca gct 835  
 Glu Glu Pro Ile Ala Ala Ala Lys Asn His Gly Lys Thr Pro Ala  
 230 235 240 245  
  
 cag gtt gtt atc cgt tgg cac ctg cag aac ggt ttc gtt gtg ttc ccc 883  
 Gln Val Val Ile Arg Trp His Leu Gln Asn Gly Phe Val Val Phe Pro  
 250 255 260  
  
 aag act gtg act aag agc cgc atg gtg gaa aac atc gac gtg ttt gat 931  
 Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn Ile Asp Val Phe Asp  
 265 270 275  
  
 ttc gaa ctc agt gat gag gag atg gct gcg atc act gct ctt gag cgc 979  
 Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile Thr Ala Leu Glu Arg  
 280 285 290  
  
 aat gat cgt ggt ggt tca cac ccg aat gat ctg aac tagaaataag  
 1025  
 Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu Asn  
 295 300 305  
  
 gtaaggccct gca  
 1038

&lt;210&gt; 860

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 860

Met Ser Val Val Gly Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu  
 1 5 10 15  
  
 Arg Asp Lys Leu Met Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser  
 20 25 30  
  
 Lys Ser Glu Gly Ile Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile  
 35 40 45  
  
 Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu  
 50 55 60  
  
 Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr  
 65 70 75 80  
  
 Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys  
 85 90 95  
  
 Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn  
 100 105 110  
  
 Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys  
 115 120 125  
  
 Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro  
 130 135 140



Lys Asn Asp Asn Tyr Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly  
 145 150 155 160  
 Asp Arg Ala Arg Ser Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu  
 165 170 175  
 Glu Lys Leu Leu Ala Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile  
 180 185 190  
 Glu Leu His Pro Ala Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu  
 195 200 205  
 Ala Ala Gly Ile Thr Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg  
 210 215 220  
 Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Lys Asn His  
 225 230 235 240  
 Gly Lys Thr Pro Ala Gln Val Val Ile Arg Trp His Leu Gln Asn Gly  
 245 250 255  
 Phe Val Val Phe Pro Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn  
 260 265 270  
 Ile Asp Val Phe Asp Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile  
 275 280 285  
 Thr Ala Leu Glu Arg Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu  
 290 295 300  
 Asn  
 305

<210> 861  
 <211> 1683  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1660)  
 <223> RXS00389

<400> 861  
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 tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115  
 Met Ile Thr Ala Thr  
 1 5  
 gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163  
 Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys  
 10 15 20  
 aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211  
 Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn  
 25 30 35  
 cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259

Pro	Ser	Tyr	Ser	Leu	Ala	Asn	Ser	Ala	Gln	Leu	Arg	Ala	Ala	Thr	Thr	
	40						45					50				
tcg	gcg	aag	cga	gct	ttt	gaa	agc	tac	cga	ctc	act	act	cca	gag	gtt	307
Ser	Ala	Lys	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Leu	Thr	Thr	Pro	Glu	Val	
	55					60					65					
aga	gca	gat	ttc	ctg	gat	tcc	atc	gct	gac	aac	atc	gat	gcg	cta	tcc	355
Arg	Ala	Asp	Phe	Leu	Asp	Ser	Ile	Ala	Asp	Asn	Ile	Asp	Ala	Leu	Ser	
	70				75					80					85	
ggc	gag	atc	gtg	caa	cgg	gcg	agc	ctg	gag	aca	ggt	ttg	gga	act	acc	403
Gly	Glu	Ile	Val	Gln	Arg	Ala	Ser	Leu	Glu	Thr	Gly	Leu	Gly	Thr	Thr	
				90					95					100		
cga	ctc	aca	ggc	gaa	gta	gcc	cgc	acc	agc	aac	cag	ctc	cgc	ctg	ttt	451
Arg	Leu	Thr	Gly	Glu	Val	Ala	Arg	Thr	Ser	Asn	Gln	Leu	Arg	Leu	Phe	
			105					110					115			
gca	gaa	acc	gtg	aga	agc	gga	cag	ttc	cac	cga	gta	cgc	att	gaa	cga	499
Ala	Glu	Thr	Val	Arg	Ser	Gly	Gln	Phe	His	Arg	Val	Arg	Ile	Glu	Arg	
		120					125					130				
gga	ccg	cgg	att	gat	ctt	cgc	cag	cgt	cag	ggt	ccg	ttg	gga	cca	gtc	547
Gly	Pro	Arg	Ile	Asp	Leu	Arg	Gln	Arg	Gln	Val	Pro	Leu	Gly	Pro	Val	
	135					140					145					
gcg	gta	ttc	ggg	gca	agc	aac	ttc	ccc	gtc	gct	ttc	tct	act	gct	ggc	595
Ala	Val	Phe	Gly	Ala	Ser	Asn	Phe	Pro	Val	Ala	Phe	Ser	Thr	Ala	Gly	
	150				155					160					165	
ggc	gat	aca	gca	tca	gcg	ttg	gct	gca	ggc	tgc	cct	gtg	ggt	ttt	aag	643
Gly	Asp	Thr	Ala	Ser	Ala	Leu	Ala	Ala	Gly	Cys	Pro	Val	Val	Phe	Lys	
			170						175					180		
gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val	
			185					190					195			
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggt	gtg	ttt	aac	ctt	739
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu	
		200					205					210				
gtc	tac	ggc	cgt	ggc	gtg	gaa	att	ggc	cag	gag	ctg	gct	gcy	gat	ccg	787
Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro	
	215					220					225					
aat	atc	acg	gca	atc	ggt	ttt	acc	ggt	tca	cgc	cag	ggt	ggt	ttg	gca	835
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala	
	230				235					240				245		
ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	gtt	ccc	gtt	cca	gtc	ttt	gca	883
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala	
				250				255						260		
gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcy	ctg	gcg	931
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala	
			265				270					275				
gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcy	ttt	acc	gct	tcc	gtc	979
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val	

280	285	290
acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc 1027		
Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile 295 300 305		
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa 1075		
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys 310 315 320 325		
ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag 1123		
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln 330 335 340		
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa 1171		
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys 345 350 355		
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg 1219		
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro 360 365 370		
gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg 1267		
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu 375 380 385		
cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc 1315		
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser 390 395 400 405		
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca 1363		
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr 410 415 420		
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt 1411		
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu 425 430 435		
atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459		
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp 440 445 450		
cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507		
Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr 455 460 465		
ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555		
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile 470 475 480 485		

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg  
1603

Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu  
490 495 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa  
1651

Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu  
505 510 515

ata gac cgt taatagctgg tctttacatt tgc  
1683

Ile Asp Arg  
520

<210> 862

<211> 520

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 862

Met Ile Thr Ala Thr Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu  
1 5 10 15

Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr  
20 25 30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu  
35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu  
50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn  
65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr  
85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn  
100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg  
115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val  
130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala  
145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys  
165 170 175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu  
180 185 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala  
195 200 205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu  
 210 215 220  
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg  
 225 230 235 240  
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro  
 245 250 255  
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe  
 260 265 270  
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala  
 275 280 285  
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro  
 290 295 300  
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala  
 305 310 315 320  
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr  
 325 330 335  
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala  
 340 345 350  
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu  
 355 360 365  
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu  
 370 375 380  
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val  
 385 390 395 400  
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu  
 405 410 415  
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln  
 420 425 430  
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val  
 435 440 445  
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile  
 450 455 460  
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val  
 465 470 475 480  
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr  
 485 490 495  
 Phe Pro Ala Glu Leu Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp  
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 Ala Val Pro Arg Glu Ile Asp Arg  
 515 520

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<222> (101)..(859)
<223> RXS00419
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1191

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691  
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser  
                   185                  190                  195

gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739  
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala  
                   200                  205                  210

gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787  
 Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val  
                   215                  220                  225

cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835  
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg  
                   230                  235                  240                  245

gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg 882  
 Ala Ile Phe Arg Lys Leu Pro Phe  
                   250

<210> 864

<211> 253

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 864

Met Leu Asn Ala Val Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly  
   1                  5                  10                  15

Thr Ser Glu Ile Gly Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly  
                   20                  25                  30

Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp  
                   35                  40                  45

Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val  
                   50                  55                  60

Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp  
                   65                  70                  75                  80

Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly  
                   85                  90                  95

Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val  
                   100                  105                  110

Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu  
                   115                  120                  125

Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu  
                   130                  135                  140

Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly  
                   145                  150                  155                  160

Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala  
                   165                  170                  175

Leu Arg Gly Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val  
 180 185 190  
 Arg Thr Lys Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn  
 195 200 205  
 Arg Glu Asp Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys  
 210 215 220  
 Asp Ile Ile Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe  
 225 230 235 240  
 Gln Phe Ile Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe  
 245 250

&lt;210&gt; 865

&lt;211&gt; 1673

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1650)

&lt;223&gt; RXC00416

&lt;400&gt; 865

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Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala	
1 5 10 15	
att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac	96
Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp	
20 25 30	
cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc	144
Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly	
35 40 45	
ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga	192
Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly	
50 55 60	
tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt	240
Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly	
65 70 75 80	
tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct	288
Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala	
85 90 95	
tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg	336
Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val	
100 105 110	
gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat	384
Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn	
115 120 125	
tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg	432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met	



130	135	140	
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc			480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala			
145	150	155	160
ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc			528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe			
	165	170	175
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg			576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala			
	180	185	190
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg			624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu			
	195	200	205
ggt ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt			672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu			
	210	215	220
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac			720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His			
	225	230	235
tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca			768
Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser			
	245	250	255
agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg			816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val			
	260	265	270
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg			864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val			
	275	280	285
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac			912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn			
	290	295	300
acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc			960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala			
	305	310	315
acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat			1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr			
	325	330	335
cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc			1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr			
	340	345	350
aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa			1104
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln			
	355	360	365

gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat  
 1152  
 Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp  
 370 375 380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca  
 1200  
 Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala  
 385 390 395 400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag  
 1248  
 Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu  
 405 410 415

cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac  
 1296  
 Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr  
 420 425 430

tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg  
 1344  
 Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro  
 435 440 445

ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc  
 1392  
 Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile  
 450 455 460

cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg  
 1440  
 Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu  
 465 470 475 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc  
 1488  
 Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser  
 485 490 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg  
 1536  
 Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu  
 500 505 510

tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg  
 1584  
 Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro  
 515 520 525

gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg  
 1632  
 Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val  
 530 535 540

gtg gta acg cac aat gag taattcctca ccaaacgacc caa  
 1673  
 Val Val Thr His Asn Glu  
 545 550

<210> 866  
 <211> 550  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 866

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Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
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Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
          20             25             30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
          35             40             45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
          50             55             60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
          65             70             75             80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
          85             90             95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
          100             105             110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
          115             120             125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
          130             135             140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
          145             150             155             160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
          165             170             175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
          180             185             190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
          195             200             205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
          210             215             220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
          225             230             235             240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
          245             250             255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
          260             265             270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
          275             280             285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
  
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290	295	300
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala 305 310 315 320		
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335		
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350		
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365		
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp 370 375 380		
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala 385 390 395 400		
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu 405 410 415		
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr 420 425 430		
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro 435 440 445		
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile 450 455 460		
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu 465 470 475 480		
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser 485 490 495		
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu 500 505 510		
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro 515 520 525		
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val 530 535 540		
Val Val Thr His Asn Glu 545 550		

&lt;210&gt; 867

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1036)

&lt;223&gt; RXC02206

&lt;400&gt; 867

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ggcaggatct gctgctgcgg ctaggaggggt tatctcttca ttcacccgat ctaccgtact 60
accttatgac ctacagtagtg tgggtgggcgt gaaacagcga atg gtc ggt tca agt 115
                                         Met Val Gly Ser Ser
                                         1           5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
                        10           15           20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
                        25           30           35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
                        40           45           50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
                        55           60           65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
                        70           75           80           85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
                        90           95           100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
                        105           110           115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
                        120           125           130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
                        135           140           145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca 595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
                        150           155           160           165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
                        170           175           180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
                        185           190           195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
                        200           205           210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr

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215                      220                      225  
 gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc 835  
 Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile  
 230                      235                      240                      245  
 att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc 883  
 Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro  
 250                      255                      260  
 gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct 931  
 Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala  
 265                      270                      275  
 gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag 979  
 Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys  
 280                      285                      290  
 gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat  
 1027  
 Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp  
 295                      300                      305  
 gtc tcc ctg tgacttggtc caattacatt cac  
 1059  
 Val Ser Leu  
 310  
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 <211> 312  
 <212> PRT  
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 20                      25                      30  
 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn  
 35                      40                      45  
 Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala  
 50                      55                      60  
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn  
 65                      70                      75                      80  
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu  
 85                      90                      95  
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu  
 100                      105                      110  
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu  
 115                      120                      125  
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr  
 130                      135                      140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala  
 145 150 155 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln  
 165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro  
 180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly  
 195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser  
 210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp  
 225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly  
 245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg  
 260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu  
 275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr  
 290 295 300

Gln Ala Leu Asp Asp Val Ser Leu  
 305 310

<210> 869  
 <211> 621  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(598)  
 <223> RXS03074

<400> 869  
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 Met Thr Gln Ser Ala  
 1 5  
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20  
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35  
 ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259

Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
           40                                  45                                  50  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
           55                                  60                                  65  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
           70                                  75                                  80                                  85  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                                   90                                  95                                  100  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                                   105                                  110                                  115  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
                                   120                                  125                                  130  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                                  140                                  145  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                                  155                                  160                                  165  
 cag taatttggtt tgacgacgca gta 621  
 Gln

&lt;210&gt; 870

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 870

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 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                                  25                                  30  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                                  40                                  45  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                                  55                                  60  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                                  70                                  75                                  80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
                                   85                                  90                                  95  
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr



100	105	110
Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr		
115	120	125
Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe		
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Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr		
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Glu Ala Pro Ile Lys Gln		
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(598)  
 <223> FRXA02906

<400> 871  
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 Met Thr Gln Ser Ala  
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cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
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gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
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ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
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ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
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gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499

Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
           120                          125                          130  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                          155                          160                          165  
 cag taatttgttt tgacgacgca gta 621  
 Gln

<210> 872  
 <211> 166  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 872  
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           20                          25                          30  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                          40                          45  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
       50                          55                          60  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
       65                          70                          75                          80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
           85                          90                          95  
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
           100                          105                          110  
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
           115                          120                          125  
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
       130                          135                          140  
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
       145                          150                          155                          160  
 Glu Ala Pro Ile Lys Gln  
           165

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1729)

&lt;223&gt; RXA02315

&lt;400&gt; 873

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gaatcgatc cgtaacctga gacgatctag actgttgctgc atg tcc agc acg cca 115
Met Ser Ser Thr Pro
1 5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctg gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
10 15 20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tgc ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
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ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctg 403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
105 110 115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
120 125 130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547
Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly
135 140 145

gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg 595
Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu
150 155 160 165

gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643
Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser
170 175 180

tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691
Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly
185 190 195

gag cac acc ctg gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739

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Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
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Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
	215					220					225						
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
230					235					240					245		
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883	
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
			250						255					260			
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
			265					270					275				
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
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ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc		
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Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
		295				300					305						
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt		
1075																	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		
310					315					320					325		
gcg	gcc	gat	ggt	gtg	cgt	gac	gtc	ctg	gac	aac	caa	gaa	ttc	ggt	ttc		
1123																	
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe		
				330					335					340			
acc	ggc	ctc	cat	ggt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc		
1171																	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly		
			345					350					355				
gat	act	ctc	ttt	gct	gca	gca	tcc	aac	tca	atc	cgt	gac	ctc	tcc	ctg		
1219																	
Asp	Thr	Leu	Phe	Ala	Ala	Ala	Ser	Asn	Ser	Ile	Arg	Asp	Leu	Ser	Leu		
		360					365					370					
gtg	ggt	atg	cct	ttt	gat	ggc	gtg	gat	acc	ttc	tcc	cca	cga	ggt	gtc		
1267																	
Val	Gly	Met	Pro	Phe	Asp	Gly	Val	Asp	Thr	Phe	Ser	Pro	Arg	Gly	Val		
	375					380					385						
gca	ggc	att	gat	ggt	tct	ggt	gct	caa	gca	atc	ggc	act	tca	ctt	gct		
1315																	
Ala	Gly	Ile	Asp	Gly	Ser	Val	Ala	Gln	Ala	Ile	Gly	Thr	Ser	Leu	Ala		
390					395					400					405		
gtg	cag	tcc	cgc	cac	ccc	gat	gaa	atc	cgc	gcg	cca	cgc	act	gtg	gcc		
1363																	
Val	Gln	Ser	Arg	His	Pro	Asp	Glu	Ile	Arg	Ala	Pro	Arg	Thr	Val	Ala		

410	415	420
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ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac 1459		
Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn 440 445 450		
gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt 1507		
Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly 455 460 465		
ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc 1555		
Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser 470 475 480 485		
atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac 1603		
Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp 490 495 500		
aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc 1651		
Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser 505 510 515		
gga ttc acc att att gaa gct tgc acc gtc cga gat acc cgc cgt gca 1699		
Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala 520 525 530		
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Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His 35 40 45		

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala  
 50 55 60  
 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala  
 65 70 75 80  
 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile  
 85 90 95  
 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr  
 100 105 110  
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala  
 115 120 125  
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu  
 130 135 140  
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala  
 145 150 155 160  
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu  
 165 170 175  
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val  
 180 185 190  
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala  
 195 200 205  
 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr  
 210 215 220  
 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu  
 225 230 235 240  
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro  
 245 250 255  
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu  
 260 265 270  
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr  
 275 280 285  
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr  
 290 295 300  
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser  
 305 310 315 320  
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn  
 325 330 335  
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp  
 340 345 350  
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile  
 355 360 365  
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe

370					375					380					
Ser 385	Pro	Arg	Gly	Val	Ala 390	Gly	Ile	Asp	Gly	Ser 395	Val	Ala	Gln	Ala	Ile 400
Gly	Thr	Ser	Leu	Ala 405	Val	Gln	Ser	Arg	His 410	Pro	Asp	Glu	Ile	Arg 415	Ala
Pro	Arg	Thr	Val 420	Ala	Leu	Leu	Gly	Asp 425	Leu	Ser	Phe	Leu	His 430	Asp	Ile
Gly	Gly	Leu 435	Leu	Ile	Gly	Pro	Asp 440	Glu	Pro	Arg	Pro	Glu 445	Asn	Leu	Thr
Ile 450	Val	Val	Ser	Asn	Asp	Asn 455	Gly	Gly	Gly	Ile	Phe 460	Glu	Leu	Leu	Glu
Thr 465	Gly	Ala	Asp	Gly	Leu 470	Arg	Pro	Asn	Phe	Glu 475	Arg	Ala	Phe	Gly	Thr 480
Pro	His	Asp	Ala	Ser 485	Ile	Ala	Asp	Leu	Cys 490	Ala	Gly	Tyr	Gly	Ile 495	Glu
His	Gln	Val	Val 500	Asp	Asn	Leu	Gln	Asp 505	Leu	Ile	Ile	Ala	Leu 510	Val	Asp
Thr	Thr	Glu 515	Val	Ser	Gly	Phe	Thr 520	Ile	Ile	Glu	Ala	Ser 525	Thr	Val	Arg
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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA02319
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Met Ser Asn Tyr Ser
1 5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
10 15 20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
25 30 35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn
40 45 50

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gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac	307
Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His	
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Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly	
70 75 80 85	
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Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln	
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cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc	451
Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg	
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gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa	499
Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys	
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Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg	
135 140 145	
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Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly	
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Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg	
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Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp	
185 190 195	
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Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn	
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gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg	787
Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met	
215 220 225	
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Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu	
230 235 240 245	
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc	883
Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr	
250 255 260	
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc	931
Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu	
265 270 275	
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg	979
Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met	
280 285 290	



acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa  
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct  
1077

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1080

<210> 876

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 876

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35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met  
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr  
210 215 220

Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp  
 225 230 235 240  
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn  
 245 250 255  
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu  
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 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr  
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 <213> Corynebacterium glutamicum

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 <223> RXS00393

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 Met Ser His Thr Glu  
 1 5  
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
 10 15 20  
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly  
 25 30 35  
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259  
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
 40 45 50  
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307  
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp  
 55 60 65  
 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355  
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu  
 70 75 80 85  
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403  
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala  
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc gcc acc gcg ctg agc 451  
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser  
 105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc gcc atc ctg tgt gtg ctg 499  
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu  
 120 125 130

gcc gcg tgg ttc tac acc gcc ggt aaa aat cct tat ggt tac cgc ggg 547  
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly  
 135 140 145

ctc gcc gag att gct gtg ttc atc ttc ttc gcc ctc gtc gcg gtc atg 595  
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met  
 150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643  
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala  
 170 175 180

gcc gca gtt gcc gtg ggg tgg atg tct gct gcc gtg aac ttg gcc aac 691  
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn  
 185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu  
 200 205 210

gcg gtc cgc ctg gcc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
 215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
 230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883  
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala  
 250 255 260

ggg ccg atc cgc aac aac gcc acc gcc aag gat ctc atc ccc gtc atc 931  
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile  
 265 270 275

gcc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg gcc ctg 979  
 Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu  
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gca tta gcg ttt agc taaaacgctt ttgcagctc ccc  
 1017  
 Ala Leu Ala Phe Ser  
 295

<210> 878  
 <211> 298  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 878  
 Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp

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Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val	20	25	30
Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala	275	280	285
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser	290	295	

&lt;210&gt; 879

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(982)

&lt;223&gt; FRXA00393

&lt;400&gt; 879

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aattgcgcga tcgagtatgt gatggggaaa gatagagggtt atg tct cac acg gaa 115
                                         Met Ser His Thr Glu
                                         1                               5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
                        10                               15                               20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
                        25                               30                               35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
                        40                               45                               50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
                        55                               60                               65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
                        70                               75                               80                               85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
                        90                               95                               100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
                        105                               110                               115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
                        120                               125                               130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
                        135                               140                               145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
                        150                               155                               160                               165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
                        170                               175                               180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
                        185                               190                               195

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aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu  
 200 205 210  
 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
 215 220 225  
 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
 230 235 240 245  
 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883  
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala  
 250 255 260  
 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931  
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser  
 265 270 275  
 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979  
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 280 285 290

cat tagcggttag ctaaaacgct ttt  
 1005  
 His

<210> 880  
 <211> 294  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 880  
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 20 25 30  
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp  
 35 40 45  
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
 50 55 60  
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
 65 70 75 80  
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
 85 90 95  
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
 100 105 110  
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
 115 120 125  
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro

130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly 145 150 155 160		
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser 165 170 175		
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly 180 185 190		
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr 195 200 205		
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys 210 215 220		
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu 225 230 235 240		
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu 245 250 255		
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp 260 265 270		
Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro 275 280 285		
Cys Ser Arg Ala Trp His 290		

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(820)  
 <223> RXA00391

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 Leu Leu Arg Asp Ser  
 1 5  
 caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc 163  
 Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala  
 10 15 20  
 act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg 211  
 Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu  
 25 30 35  
 aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa 259  
 Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu  
 40 45 50

ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307  
 Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln  
 55 60 65

gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355  
 Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp  
 70 75 80 85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403  
 Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu  
 90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451  
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln  
 105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499  
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu  
 120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547  
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg  
 135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595  
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser  
 150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643  
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly  
 170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691  
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met  
 185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739  
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn  
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787  
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile  
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 230 235 240

tgc 843

<210> 882  
 <211> 240  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 882  
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Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala  
 20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln  
 35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His  
 50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu  
 65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala  
 85 90 95

Gly Ala Ala Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser  
 100 105 110

Leu Thr Pro Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile  
 115 120 125

Glu Ala Leu Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu  
 130 135 140

Ser Lys Gln Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val  
 145 150 155 160

Thr Thr Tyr Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly  
 165 170 175

Lys Pro Ile Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu  
 180 185 190

Leu Gly Gly Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His  
 195 200 205

Pro Asp Phe Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu  
 210 215 220

Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 225 230 235 240

&lt;210&gt; 883

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(361)

&lt;223&gt; RXS02908

&lt;400&gt; 883

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gtgactggtc gcgtggatac ccgtcattga ttccggtgga ttg aag ttg cac cca 115  
 Leu Lys Leu His Pro

											1						5		
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg	163																		
Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala																			
10                                15                                20																			
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc	211																		
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala																			
25                                30                                35																			
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac	259																		
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp																			
40                                45                                50																			
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct	307																		
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser																			
55                                60                                65																			
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag	355																		
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys																			
70                                75                                80                                85																			
ctg ttt tagtcttcat tcttgctggc tgc	384																		
Leu Phe																			

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<210> 884
<211> 87
<212> PRT
<213> Corynebacterium glutamicum
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<400> 884

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Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
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Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
          20           25           30
Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
          35           40           45
Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
 50           55           60
Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
 65           70           75           80
Arg Ala Ile Ala Lys Leu Phe
          85

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<210> 885
<211> 705
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(682)  
<223> RXA00997
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&lt;400&gt; 885

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gcaccatggg gctgaacaag tagccctata ctcgggcacc atg act aca tgg aaa 115
                                     Met Thr Thr Trp Lys
                                     1 5
gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
                                     10 15 20
tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
                                     25 30 35
ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
                                     40 45 50
tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
                                     55 60 65
gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
                                     70 75 80 85
gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
                                     90 95 100
atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
                                     105 110 115
ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499
Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
                                     120 125 130
cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
                                     135 140 145
cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
                                     150 155 160 165
ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
                                     170 175 180
caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692
Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
                                     185 190
atcttgcacc tga 705

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&lt;210&gt; 886

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 886

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Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu
  1           5           10           15

Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile
          20           25           30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys
          35           40           45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser
          50           55           60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile
          65           70           75           80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp
          85           90           95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser
          100          105          110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala
          115          120          125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile
          130          135          140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val
          145          150          155          160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp
          165          170          175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr
          180          185          190

Lys Lys

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&lt;210&gt; 887

&lt;211&gt; 861

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(838)

&lt;223&gt; RXA02189

&lt;400&gt; 887

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aatggcaaaa atgggcacat acgatactga tgggaccaat gggaaaacct caagccacca 60

attgagccag ttctctcaag caaaccgata ctggtgggat gtg gac gcg gcc gac 115
                Val Asp Ala Ala Asp
                1           5

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tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc	163
Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly	
10 15 20	
gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt	211
Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu	
25 30 35	
ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt	259
Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly	
40 45 50	
tgc ggc tgc gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat	307
Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn	
55 60 65	
gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca	355
Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala	
70 75 80 85	
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Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu	
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ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc	451
Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala	
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Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg	
120 125 130	
gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg	547
Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met	
135 140 145	
cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc	595
Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile	
150 155 160 165	
acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc	643
Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr	
170 175 180	
ggt gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg cgg atc	691
Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile	
185 190 195	
aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca	739
Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro	
200 205 210	
gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt	787
Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly Gln Trp Ser Pro Leu	
215 220 225	
cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc	835
Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg	
230 235 240 245	
ccc taaaaaacca acggcgctca ttt	861

Pro

&lt;210&gt; 888

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 888

Val Asp Ala Ala Asp Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr  
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 Asp Ser Ala His Gly Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu  
 20 25 30  
 Lys Asp Val Arg Leu Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys  
 35 40 45  
 Ile Leu Glu Ile Gly Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala  
 50 55 60  
 Asn Asp Val Pro Asn Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln  
 65 70 75 80  
 Met Leu Lys Tyr Ala Gly His Asp His Asn Val His Leu Val Gln Ala  
 85 90 95  
 Asp Ala Met Ser Leu Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe  
 100 105 110  
 Ser Val Phe Gly Ala Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met  
 115 120 125  
 Lys Glu Ile Ala Arg Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser  
 130 135 140  
 Ile Thr His Pro Met Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala  
 145 150 155 160  
 Gly Leu Thr Ala Ile Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu  
 165 170 175  
 Glu Asp Glu Glu Thr Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr  
 180 185 190  
 Met Gly Ala Arg Ile Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp  
 195 200 205  
 His Leu Ile Glu Pro Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly  
 210 215 220  
 Gln Trp Ser Pro Leu Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe  
 225 230 235 240  
 Leu Ala Thr Tyr Arg Pro  
 245

&lt;210&gt; 889

&lt;211&gt; 813

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(790)

&lt;223&gt; RXA02311

&lt;400&gt; 889

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aataacctcc cactaaagct cctggggttag actcgaacgc gtg gct aaa gca gat 115
                                   Val Ala Lys Ala Asp
                                   1 5
tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163
Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly
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Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg
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gtg tgg cga aag cgc act agg cag cgc ctg gac ctc aag cca ggg gag 259
Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu
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aag gtg ctt gat cta gct gca gga aca gcc gtt tcc acc gtg gag ttg 307
Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu
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Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met
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ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403
Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly
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atg cag ttg ccg ttt gca gac aac agc ttt gat gct gtg acc att tct 451
Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp Ala Val Thr Ile Ser
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tat ggt ctg cgc aat att cac gat ttc cgc gct ggc ctg aaa gaa atg 499
Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala Gly Leu Lys Glu Met
      120      125      130
gcc cgc gtg act aaa cct ggt gga cgc ctc acc gtg gcg gag ttc tcc 547
Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr Val Ala Glu Phe Ser
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acc ccc gtg atc cct gtg ttc ggc acc gtg tac aag gag tac ctc atg 595
Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr Lys Glu Tyr Leu Met
      150      155      160      165
cgc ctg ctg ccc cag gcg gcg cgc gca gta tcg tcc aac ccg gag gcc 643
Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser Ser Asn Pro Glu Ala
      170      175      180
tac att tac ctg gct gat tcc atc cgc gca tgg cct agc cag gcg gaa 691
Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp Pro Ser Gln Ala Glu

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185	190	195	
cta gca cgg gag atc aac cag aat ggt tgg tca gat tgc ggt tgg cag			739
Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser Asp Cys Gly Trp Gln			
200	205	210	
aac ctg acc ttc ggc atc gtc gcg ctg cac tcg gcg att aaa cca gag			787
Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser Ala Ile Lys Pro Glu			
215	220	225	
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Asn			
230			
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<211> 230			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 890			
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Phe Gly Gln Asp Arg Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp			
35	40	45	
Leu Lys Pro Gly Glu Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val			
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Ser Thr Val Glu Leu Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp			
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Phe Ser Gln Gly Met Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys			
85	90	95	
Val Val Gly Asp Gly Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp			
100	105	110	
Ala Val Thr Ile Ser Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala			
115	120	125	
Gly Leu Lys Glu Met Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr			
130	135	140	
Val Ala Glu Phe Ser Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr			
145	150	155	160
Lys Glu Tyr Leu Met Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser			
165	170	175	
Ser Asn Pro Glu Ala Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp			
180	185	190	
Pro Ser Gln Ala Glu Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser			
195	200	205	
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210 215 220

Ala Ile Lys Pro Glu Asn  
225 230

<210> 891  
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<212> DNA  
<213> Corynebacterium glutamicum

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<223> RXN02912

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Val Thr Ser Pro Glu  
1 5

tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac 163  
Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly Arg Ala Glu Ala Tyr  
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cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc 211  
His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln Phe Glu Arg Pro Ile  
25 30 35

tgg gaa aag gtg tgg tgc aag gct ttg cct atc gtg tgc gaa gaa gcg 259  
Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile Val Ser Glu Glu Ala  
40 45 50

gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt 307  
Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly Tyr Val Thr His Leu  
55 60 65

cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa 355  
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu  
70 75 80 85

atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tgc acg ggt 403  
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly  
90 95 100

cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc 451  
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe  
105 110 115

cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act 499  
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr  
120 125 130

ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa 547  
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys  
135 140 145

cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc 595  
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly

150	155	160	165	
att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc				643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe				
	170	175	180	
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg				691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr				
	185	190	195	
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc				739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu				
	200	205	210	
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag				787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln				
	215	220	225	
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc				835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe				
	230	235	240	245
agg gga att aaa tcc agt tagtgctgtt ttaagcggtc gag				876
Arg Gly Ile Lys Ser Ser				
	250			

&lt;210&gt; 892

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 892

Val Thr Ser Pro Glu Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly				
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Arg Ala Glu Ala Tyr His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln				
	20	25	30	
Phe Glu Arg Pro Ile Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile				
	35	40	45	
Val Ser Glu Glu Ala Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly				
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Tyr Val Thr His Leu Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val				
	65	70	75	80
Asp Gly Ser Glu Glu Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu				
	85	90	95	
Arg Arg Ser Thr Gly Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala				
	100	105	110	
His Asp Pro Glu Phe Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg				
	115	120	125	
Tyr Val Leu Trp Thr Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp				
	130	135	140	
Val Ser Leu Leu Lys Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala				

145	150	155	160
Trp Tyr Pro Lys Gly Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp			
	165	170	175
Gly Pro Ser Ala Phe Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn			
	180	185	190
Leu Pro Met Ser Thr Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe			
	195	200	205
His Asn Ala Gly Leu Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu			
	210	215	220
Ala Glu Leu Asp Gln Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr			
	225	230	235
			240
Pro Gln Phe Leu Phe Arg Gly Ile Lys Ser Ser			
	245	250	

&lt;210&gt; 893

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(562)

&lt;223&gt; RXS00998

&lt;400&gt; 893

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                                         Met Thr Ser Arg Asp
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gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga 163
Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg
                               10                               15                               20

gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211
Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly
                               25                               30                               35

ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg 259
Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg
                               40                               45                               50

gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307
Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly
                               55                               60                               65

ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355
Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser
                               70                               75                               80                               85

gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac 403
Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn
                               90                               95                               100

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aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451  
 Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala  
                   105                                  110                                  115

gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499  
 Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile  
                   120                                  125                                  130

gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547  
 Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr  
                   135                                  140                                  145

atg gtg ctg aac aag tagccctata ctcgggcacc atg 585  
 Met Val Leu Asn Lys  
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<210> 894

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 894

Met Thr Ser Arg Asp Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu  
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Leu Ala Ala Thr Arg Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn  
                   20                                  25                                  30

Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr  
                   35                                  40                                  45

Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His  
           50                                  55                                  60

Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala  
           65                                  70                                  75                                  80

Glu Ser Thr Gly Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met  
                   85                                  90                                  95

Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser  
                   100                                  105                                  110

Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr  
           115                                  120                                  125

His Leu Trp Gln Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg  
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Thr Thr Leu Arg Thr Met Val Leu Asn Lys  
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<220>

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&lt;222&gt; (101)..(1075)

&lt;223&gt; RXA01215

&lt;400&gt; 895

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                                         Met Thr Ala His Trp
                                         1 5
aaa caa aac caa aag aac ctc atg ctg ttt tcg ggt cgt gcg cac cca 163
Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro
                        10 15 20
gaa ctg gca gaa gct gta gct aaa gag ctc gac gtc aac gtc acc cca 211
Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro
                        25 30 35
atg acg gca cgc gat ttc gcc aac ggt gaa atc tac gtc cgc ttc gag 259
Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu
                        40 45 50
gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag 307
Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln
                        55 60 65
cct ctc aac aag tgg ctc atg gaa cag ctg ctg atg atc gac gct ttg 355
Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu Met Ile Asp Ala Leu
                        70 75 80 85
aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca 403
Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro
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Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala
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Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly Ala Asp Arg Ile Val
                        120 125 130
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Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly Phe Phe Asp Gly Pro
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gtc gat cac atg cac gcc atg ccg atc ctc acc gat cac atc aag gaa 595
Val Asp His Met His Ala Met Pro Ile Leu Thr Asp His Ile Lys Glu
                        150 155 160 165
aac tac aac ctg gac aac atc tgc gtg gtc tcc cct gac gca ggt cgc 643
Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser Pro Asp Ala Gly Arg
                        170 175 180
gtg aag gtt gca gag aag tgg gct aac acc ttg ggc gat gcc cca atg 691
Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu Gly Asp Ala Pro Met
                        185 190 195
gcg ttc gtg cac aag acc cgc tcc acc gag gta gca aac cag gtt gtc 739
Ala Phe Val His Lys Thr Arg Ser Thr Glu Val Ala Asn Gln Val Val

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215	220	225	
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Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala Gly Ala Val Gly Val			
230	235	240	245
ctg aag aag gct ggc gca aag tca gtc gtc atc gcc tgc acc cac ggt			883
Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile Ala Cys Thr His Gly			
250	255	260	
gtg ttc tct gac cca gcc cgc gag cgc ctg tct gca tgc ggt gct gaa			931
Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser Ala Cys Gly Ala Glu			
265	270	275	
gaa gtc atc acc acc gac acc ctg cca cag tcc acc gag ggc tgg agc			979
Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser Thr Glu Gly Trp Ser			
280	285	290	
aac ctg acc gtt ttg tgc atc gca ccg ctg ctg gct cgc acc atc aac			
1027			
Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu Ala Arg Thr Ile Asn			
295	300	305	
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Tyr Val Arg Phe Glu Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu			
50	55	60	
Gln Ser His Thr Gln Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu			
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Met Ile Asp Ala Leu Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile			
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Leu Pro Phe Tyr Pro Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg			

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Glu	Pro	Ile	Ser	Ala	Arg	Leu	Ile	Ala	Asp	Leu	Met	Leu	Thr	Ala	Gly
	115						120					125			
Ala	Asp	Arg	Ile	Val	Ser	Val	Asp	Leu	His	Thr	Asp	Gln	Ile	Gln	Gly
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Phe	Phe	Asp	Gly	Pro	Val	Asp	His	Met	His	Ala	Met	Pro	Ile	Leu	Thr
	145					150					155				160
Asp	His	Ile	Lys	Glu	Asn	Tyr	Asn	Leu	Asp	Asn	Ile	Cys	Val	Val	Ser
				165					170					175	
Pro	Asp	Ala	Gly	Arg	Val	Lys	Val	Ala	Glu	Lys	Trp	Ala	Asn	Thr	Leu
		180						185					190		
Gly	Asp	Ala	Pro	Met	Ala	Phe	Val	His	Lys	Thr	Arg	Ser	Thr	Glu	Val
		195					200					205			
Ala	Asn	Gln	Val	Val	Ala	Asn	Arg	Val	Val	Gly	Asp	Val	Asp	Gly	Lys
	210					215					220				
Asp	Cys	Val	Leu	Leu	Asp	Asp	Met	Ile	Asp	Thr	Gly	Gly	Thr	Ile	Ala
	225					230					235				240
Gly	Ala	Val	Gly	Val	Leu	Lys	Lys	Ala	Gly	Ala	Lys	Ser	Val	Val	Ile
			245						250					255	
Ala	Cys	Thr	His	Gly	Val	Phe	Ser	Asp	Pro	Ala	Arg	Glu	Arg	Leu	Ser
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		275						280				285			
Thr	Glu	Gly	Trp	Ser	Asn	Leu	Thr	Val	Leu	Ser	Ile	Ala	Pro	Leu	Leu
	290					295					300				
Ala	Arg	Thr	Ile	Asn	Glu	Ile	Phe	Glu	Asn	Gly	Ser	Val	Thr	Thr	Leu
	305					310					315				320
Phe	Glu	Gly	Glu	Ala											
				325											

&lt;210&gt; 897

&lt;211&gt; 1470

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1447)

&lt;223&gt; RXN00558

&lt;400&gt; 897

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tcgaaactta cctactttgg cctcttcgca cttcagcacc gtg gtc aag aag ccc 115  
Val Val Lys Lys Pro

1

5

gcg ggc atc gca gta ggc gat ggc gaa cag atc ctg gtt ttc aaa gat	163
Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp	
10 15 20	
ttg ggc cta gtc tcc caa gtt ttc gac caa cca att ctg gaa tcc ctc	211
Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu	
25 30 35	
cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga	259
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly	
40 45 50	
aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc	307
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly	
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acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag	355
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu	
70 75 80 85	
ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag	403
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys	
90 95 100	
cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat	451
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His	
105 110 115	
gac gga aat aat ctc ttt gat tcc gcc aag gaa ctc ctc ccc agc gtc	499
Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val	
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aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca	547
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala	
135 140 145	
gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag	595
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu	
150 155 160 165	
cgc ggc tgg gta gtc gca tct gaa acc gca gcg ctc gac atc gta ggt	643
Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
170 175 180	
gcc tcg cat gtg cgc gag gtc gaa cca ggc gaa ctg att gct atc gac	691
Ala Ser His Val Arg Glu Val Glu Pro Gly Glu Leu Ile Ala Ile Asp	
185 190 195	
gaa tcc ggc ctc aag tcc gca cga ttc gcc gag aca acc cgc aaa ggt	739
Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
200 205 210	
tgc gtc ttc gaa tac gtt tac ctg gct cgt cca gac tcc gtg atc aag	787
Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	



gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca	883
Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser	
250 255 260	
ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc	931
Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe	
265 270 275	
ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag	979
Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln	
280 285 290	
cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca	
1027	
Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro	
295 300 305	
ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc	
1075	
Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser	
310 315 320 325	
atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa	
1123	
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330 335 340	
gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa	
1171	
Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys	
345 350 355	
tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att	
1219	
Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile	
360 365 370	
gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc	
1267	
Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val	
375 380 385	
cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc	
1315	
Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser	
390 395 400 405	
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1363	
Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu Leu Cys Ile Ala Cys	
410 415 420	
ttc gac ggc aaa tac ccc atg ggt ctg cca cag gga aac agc aac gca	
1411	
Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln Gly Asn Ser Asn Ala	
425 430 435	
gac cta gtc cgc aag atg caa gca acc gcc tca agt taagatcggg	
1457	
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440 445	

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1470

<210> 898

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 898

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Leu	Val	Phe	Lys	Asp	Leu	Gly	Leu	Val	Ser	Gln	Val	Phe	Asp	Gln	Pro	20	25	30	
Ile	Leu	Glu	Ser	Leu	Arg	Gly	Asn	Ile	Ala	Ile	Gly	His	Thr	Arg	Tyr	35	40	45	
Thr	Thr	Ala	Gly	Gly	Asn	Thr	Trp	Glu	Asn	Ala	Gln	Pro	Met	Phe	Arg	50	55	60	
Met	Ala	Pro	Asp	Gly	Thr	Asp	Ile	Ala	Leu	Gly	His	Asn	Gly	Asn	Leu	65	70	75	80
Ile	Asn	Tyr	Ile	Glu	Leu	Leu	Asp	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Val	85	90	95	
Asp	Pro	Ala	Lys	Lys	Pro	Ser	Asp	Thr	Asp	Val	Leu	Thr	Gly	Leu	Leu	100	105	110	
Ala	Ser	Gly	Val	His	Asp	Gly	Asn	Asn	Leu	Phe	Asp	Ser	Ala	Lys	Glu	115	120	125	
Leu	Leu	Pro	Ser	Val	Lys	Gly	Ala	Tyr	Cys	Leu	Thr	Phe	Thr	Asp	Gly	130	135	140	
His	Thr	Leu	Tyr	Ala	Ala	Arg	Asp	Pro	Phe	Gly	Ile	Arg	Pro	Leu	Ser	145	150	155	160
Ile	Gly	Arg	Leu	Glu	Arg	Gly	Trp	Val	Val	Ala	Ser	Glu	Thr	Ala	Ala	165	170	175	
Leu	Asp	Ile	Val	Gly	Ala	Ser	His	Val	Arg	Glu	Val	Glu	Pro	Gly	Glu	180	185	190	
Leu	Ile	Ala	Ile	Asp	Glu	Ser	Gly	Leu	Lys	Ser	Ala	Arg	Phe	Ala	Glu	195	200	205	
Thr	Thr	Arg	Lys	Gly	Cys	Val	Phe	Glu	Tyr	Val	Tyr	Leu	Ala	Arg	Pro	210	215	220	
Asp	Ser	Val	Ile	Lys	Gly	Arg	Asn	Val	Asn	Glu	Ala	Arg	Leu	Glu	Ile	225	230	235	240
Gly	Arg	Lys	Leu	Ala	Ala	Glu	Ala	Pro	Ala	Val	Gly	Asp	Leu	Val	Ile	245	250	255	
Pro	Thr	Pro	Glu	Ser	Gly	Thr	Pro	Ala	Ala	Val	Gly	Phe	Ala	Gln	Ala	260	265	270	

Ser Gly Ile Pro Phe Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly  
 275 280 285

Arg Thr Phe Ile Gln Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg  
 290 295 300

Leu Lys Leu Asn Pro Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val  
 305 310 315 320

Val Val Asp Asp Ser Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile  
 325 330 335

Arg Met Leu Arg Glu Ala Gly Ala Ala Glu Val His Val Arg Ile Ala  
 340 345 350

Ser Pro Pro Val Lys Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr  
 355 360 365

Pro Gly Glu Leu Ile Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu  
 370 375 380

Met Val Glu Ala Val Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr  
 385 390 395 400

Val Ser Ile Asp Ser Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu  
 405 410 415

Leu Cys Ile Ala Cys Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln  
 420 425 430

Gly Asn Ser Asn Ala Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser  
 435 440 445

Ser

<210> 899  
 <211> 524  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (61)..(501)  
 <223> FRXA00558

<400> 899  
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gtg gtc aag aag ccc ggc ggc atc gca gta ggc gat ggc gaa cag atc 108  
 Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile  
 1 5 10 15

ctg gtt ttc aaa gat ttg ggc cta gtc tcc caa gtt ttc gac caa cca 156  
 Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro  
 20 25 30

att ctg gaa tcc ctc cgc gga aac atc gcc atc gga cac acc cga tac 204  
 Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr

35	40	45	
acc acc gcc ggc gga aac acc tgg gaa aat gcc cag cct atg ttc cgc			252
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
atg gca cca gat ggc acc gat atc gcc ctt gga cac aac ggc aac ctg			300
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
att aat tac atc gag ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc			348
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
gat ccc gcc aag aag cca tca gat acc gat gtg ctc act gga ctg ctc			396
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
gca agc ggc gtc cat gac gga aat aat ctc ttt gat tcc gcc aag gaa			444
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	
ctc ctc ccc agc gtc aag gga gcc tac tgc ctc acc ttc acc gac gga			492
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly			
130	135	140	
cac acc ctg taagcagcgc gtgatccatt cgg			524
His Thr Leu			
145			
<210> 900			
<211> 147			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 900			
Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile			
1	5	10	15
Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro			
20	25	30	
Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr			
35	40	45	
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	

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His Thr Leu  
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<210> 901  
 <211> 1386  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1363)  
 <223> RXN00626

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 Met Arg Ile Leu Val  
 1 5  
 atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act 163  
 Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr  
 10 15 20  
 gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt 211  
 Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu  
 25 30 35  
 gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag 259  
 Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu  
 40 45 50  
 gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc 307  
 Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile  
 55 60 65  
 ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg 355  
 Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala  
 70 75 80 85  
 gcg ggt atc gct gtg ttt ggt cct aac aag gac gct gct cgt atc gag 403  
 Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp Ala Ala Arg Ile Glu  
 90 95 100  
 ggc tcc aag gct ttc gct aag gat gtc atg gct gcg cag ggt gtt cgt 451  
 Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala Ala Gln Gly Val Arg  
 105 110 115  
 act gct cat gct gag act att act cct ggt gcg tct tct gaa gat att 499  
 Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala Ser Ser Glu Asp Ile  
 120 125 130  
 gat gct gcc ata gat cgt ttc ggc cca acg tgg gtt gtc aag gat gat 547  
 Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp  
 135 140 145  
 ggt ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca 595

Gly	Leu	Ser	Ala	Gly	Lys	Gly	Val	Val	Val	Thr	Pro	Asp	Arg	Ala	Ala		
150					155					160					165		
gca	cgt	gct	cac	gta	gat	gca	gtg	ctt	gag	ggc	gga	aat	cca	gtt	ttg	643	
Ala	Arg	Ala	His	Val	Asp	Ala	Val	Leu	Glu	Gly	Gly	Asn	Pro	Val	Leu		
				170					175					180			
ctg	gag	tcc	ttc	ctt	gat	ggc	cct	gag	gtt	tcc	ctg	ttc	tgc	ctg	gtt	691	
Leu	Glu	Ser	Phe	Leu	Asp	Gly	Pro	Glu	Val	Ser	Leu	Phe	Cys	Leu	Val		
			185					190					195				
gat	ggc	gag	acg	gta	gtt	cct	ctg	ctg	cca	gcg	cag	gat	cac	aag	cgt	739	
Asp	Gly	Glu	Thr	Val	Val	Pro	Leu	Leu	Pro	Ala	Gln	Asp	His	Lys	Arg		
		200					205					210					
gcg	tac	gac	aac	gat	gag	ggc	cca	aac	act	ggt	ggc	atg	ggt	gct	tat	787	
Ala	Tyr	Asp	Asn	Asp	Glu	Gly	Pro	Asn	Thr	Gly	Gly	Met	Gly	Ala	Tyr		
	215					220					225						
gcg	ccg	ctt	cct	tgg	ctg	cct	gaa	gat	ggc	gtc	cag	cgc	att	gtc	gat	835	
Ala	Pro	Leu	Pro	Trp	Leu	Pro	Glu	Asp	Gly	Val	Gln	Arg	Ile	Val	Asp		
230					235					240				245			
gag	gtc	tgc	gtt	cct	gtt	gct	cgt	gag	atg	gtg	gca	cgt	ggt	tgc	gcg	883	
Glu	Val	Cys	Val	Pro	Val	Ala	Arg	Glu	Met	Val	Ala	Arg	Gly	Cys	Ala		
				250					255					260			
tac	tcc	ggt	ctg	ctt	tac	gca	ggt	atc	gca	tgg	ggt	gca	gaa	ggc	cct	931	
Tyr	Ser	Gly	Leu	Leu	Tyr	Ala	Gly	Ile	Ala	Trp	Gly	Ala	Glu	Gly	Pro		
			265					270					275				
gca	gta	gtg	gag	ttc	aac	tgc	cgc	ttc	ggc	gat	cca	gaa	acc	cag	gct	979	
Ala	Val	Val	Glu	Phe	Asn	Cys	Arg	Phe	Gly	Asp	Pro	Glu	Thr	Gln	Ala		
		280					285					290					
gta	ctg	gca	cta	ctg	aag	act	cct	cta	gca	gta	ctg	ctc	aac	gca	gtt		
1027																	
Val	Leu	Ala	Leu	Leu	Lys	Thr	Pro	Leu	Ala	Val	Leu	Leu	Asn	Ala	Val		
	295					300					305						
gct	act	gga	acc	ttg	gca	gag	cag	cca	gca	ctg	gag	tgg	gag	gat	gct		
1075																	
Ala	Thr	Gly	Thr	Leu	Ala	Glu	Gln	Pro	Ala	Leu	Glu	Trp	Glu	Asp	Ala		
310					315					320				325			
tac	gcc	ctg	act	gtg	gtg	ttg	gct	tct	tac	aac	tac	cca	gag	gca	cct		
1123																	
Tyr	Ala	Leu	Thr	Val	Val	Leu	Ala	Ser	Tyr	Asn	Tyr	Pro	Glu	Ala	Pro		
				330					335				340				
cgt	act	ggt	gat	gtc	atc	cgc	aac	gct	gat	gca	gat	aac	gtt	ctt	cac		
1171																	
Arg	Thr	Gly	Asp	Val	Ile	Arg	Asn	Ala	Asp	Ala	Asp	Asn	Val	Leu	His		
			345					350					355				
gct	ggt	acc	gca	ctc	aat	gct	gaa	ggc	gag	ctg	gtc	tct	gcg	ggc	ggt		
1219																	
Ala	Gly	Thr	Ala	Leu	Asn	Ala	Glu	Gly	Glu	Leu	Val	Ser	Ala	Gly	Gly		
		360					365					370					

cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg gag gct gca cgc  
 1267  
 Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu Glu Ala Ala Arg  
 375 380 385  
  
 gat aac gcg tac acc acc atc aag gac att gaa ctt gag gga agc cac  
 1315  
 Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu Glu Gly Ser His  
 390 395 400 405  
  
 tac cgc agc gat atc gca ttg gct gca tta gag ggt cgt atc tcg atc  
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 <211> 421  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 902  
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 Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys  
 35 40 45  
  
 Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser  
 50 55 60  
  
 Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala  
 65 70 75 80  
  
 Asp Ala Leu Arg Ala Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp  
 85 90 95  
  
 Ala Ala Arg Ile Glu Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala  
 100 105 110  
  
 Ala Gln Gly Val Arg Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala  
 115 120 125  
  
 Ser Ser Glu Asp Ile Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp  
 130 135 140  
  
 Val Val Lys Asp Asp Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr  
 145 150 155 160  
  
 Pro Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly  
 165 170 175  
  
 Gly Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser  
 180 185 190

Leu Phe Cys Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala  
 195 200 205  
 Gln Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly  
 210 215 220  
 Gly Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val  
 225 230 235 240  
 Gln Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val  
 245 250 255  
 Ala Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp  
 260 265 270  
 Gly Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp  
 275 280 285  
 Pro Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val  
 290 295 300  
 Leu Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu  
 305 310 315 320  
 Glu Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn  
 325 330 335  
 Tyr Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala  
 340 345 350  
 Asp Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu  
 355 360 365  
 Val Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr  
 370 375 380  
 Leu Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu  
 385 390 395 400  
 Leu Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu  
 405 410 415  
 Gly Arg Ile Ser Ile  
 420

&lt;210&gt; 903

&lt;211&gt; 364

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(364)

&lt;223&gt; FRXA00629

&lt;400&gt; 903

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 aatagcttgg atcaagtttt gcaggataaa ctgtgcaacc atg cgc att ctg gta 115  
 Met Arg Ile Leu Val



	1	5	
atc ggc tgc ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act			163
Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr	10	15	20
gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt			211
Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu	25	30	35
gga tgc atc gca act gtc cac cct ggc atc aag gct gat gat cca gag			259
Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu	40	45	50
gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc			307
Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile	55	60	65
ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg			355
Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala	70	75	80
gcg ggt atc			364
Ala Gly Ile			

&lt;210&gt; 904

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 904

Met Arg Ile Leu Val Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu	1	5	10	15
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Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro	20	25	30
---	----	----	----

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys	35	40	45
---	----	----	----

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser	50	55	60
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Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala	65	70	75	80
---	----	----	----	----

Asp Ala Leu Arg Ala Ala Gly Ile	85
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&lt;210&gt; 905

&lt;211&gt; 803

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(780)

&lt;223&gt; FRXA00626

<400> 905		
gat cgt gca gca gca cgt gct cac gta gat gca gtg ctt gag ggc gga	48	
Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly		
1 5 10 15		
aat cca gtt ttg ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg	96	
Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu		
20 25 30		
ttc ttc ctg gtt gat ggc gag acg gta gtt cct ctg ctg cca gcg cag	144	
Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln		
35 40 45		
gat cac aag cgt gcg tac gac aac gat gag ggc cca aac act ggt ggc	192	
Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly		
50 55 60		
atg ggt gct tat gcg ccg ctt cct tgg ctg cct gaa gat ggc gtc cag	240	
Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln		
65 70 75 80		
cgc att gtc gat gag gtc tgc gtt cct gtt gct cgt gag atg gtg gca	288	
Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala		
85 90 95		
cgt ggt tgc gcg tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt	336	
Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly		
100 105 110		
gca gaa ggc cct gca gta gtg gag ttc aac tgc cgc ttc ggc gat cca	384	
Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro		
115 120 125		
gaa acc cag gct gta ctg gca cta ctg aag act cct cta gca gta ctg	432	
Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu		
130 135 140		
ctc aac gca gtt gct act gga acc ttg gca gag cag cca gca ctg gag	480	
Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu		
145 150 155 160		
tgg gag gat gct tac gcc ctg act gtg gtg ttg gct tct tac aac tac	528	
Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr		
165 170 175		
cca gag gca cct cgt act ggt gat gtc atc cgc aac gct gat gca gat	576	
Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp		
180 185 190		
aac gtt ctt cac gct ggt acc gca ctc aat gct gaa ggc gag ctg gtc	624	
Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val		
195 200 205		
tct gcg ggc ggt cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg	672	
Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu		
210 215 220		
gag gct gca cgc gat aac gcg tac acc acc atc aag gac att gaa ctt	720	
Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu		
225 230 235 240		

gag gga agc cac tac cgc agc gat atc gca ttg gct gca tta gag ggt 768  
Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly  
245 250 255

cgt atc tcg atc taaaagcagt acgcagatag gct 803  
Arg Ile Ser Ile  
260

<210> 906

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 906

Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly  
1 5 10 15

Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu  
20 25 30

Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln  
35 40 45

Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly  
50 55 60

Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln  
65 70 75 80

Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala  
85 90 95

Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly  
100 105 110

Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro  
115 120 125

Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu  
130 135 140

Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu  
145 150 155 160

Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr  
165 170 175

Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp  
180 185 190

Asn Val	Leu His	Ala Gly	Thr Ala	Leu Asn	Ala Glu	Gly Glu	Leu Val
	195		200			205	

Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu  
210 215 220

Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu  
225 230 235 240

Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly  
 245 250 255

Arg Ile Ser Ile  
 260

<210> 907

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXA02623

<400> 907

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aatgatgggt ccgaggccga agaccgttaa catatctgtt gtg aat tct gac tct 115  
 Val Asn Ser Asp Ser  
 1 5

acg acc acc att gtc gtg cta gct tcc gga aca ggc acc ctc ctt cag 163  
 Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln  
 10 15 20

tca ctc att gaa gcg caa ggt acc tat tcg atc gtg ggc gtt gtc tct 211  
 Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser  
 25 30 35

gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259  
 Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp  
 40 45 50

act gca gtt gtt ccg ctt gga aaa gat cgt gca cag tgg aac cac gag 307  
 Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu  
 55 60 65

ctt gca gac gca gtt gca gta agc gac cca gat ttg gtg gtc tct gcg 355  
 Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp Leu Val Val Ser Ala  
 70 75 80 85

gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403  
 Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser  
 90 95 100

cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451  
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala  
 105 110 115

cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499  
 His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser  
 120 125 130

aca gtt cac ctt gtc gat gct ggt gtg gat acc ggc cca att att gct 547  
 Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Ile Ile Ala  
 135 140 145

caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His  
 150 155 160 165

gaa aga atc aag cag gtt gag cgt aaa ctc att gta gaa gtc ctg aac 643  
 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn  
 170 175 180

agc gtg gaa ttt tgc cgt cag ggt ggc gta caa ctc aac tgg aga ggc 691  
 Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln Leu Asn Trp Arg Gly  
 185 190 195

taaataccttc atgagc gatg atc 714

&lt;210&gt; 908

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 908

Val Asn Ser Asp Ser Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr  
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Gly Thr Leu Leu Gln Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile  
 20 25 30

Val Gly Val Val Ser Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala  
 35 40 45

Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala  
 50 55 60

Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp  
 65 70 75 80

Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu  
 85 90 95

Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro  
 100 105 110

Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val  
 115 120 125

Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr  
 130 135 140

Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp  
 145 150 155 160

Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile  
 165 170 175

Val Glu Val Leu Asn Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln  
 180 185 190

Leu Asn Trp Arg Gly  
 195

&lt;210&gt; 909

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<220>
<221> CDS
<222> (101)..(1324)
<223> RXA01442
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tgg gat tat gcg atg agc ggt gca cgc gtg gcc aac tcc cgc gtc atc 691

Trp Asp Tyr	Ala Met Ser Gly Ala Arg Val Ala Asn Ser Arg Val Ile	
185	190	195
gtg gaa gct ttc gtg gaa ttc gat tac gag atc acc ctg ttg aca gta	739	
Val Glu Ala Phe Val Glu Phe Asp Tyr Glu Ile Thr Leu Leu Thr Val		
200	205	210
agg tcc atc gat ccc acc acc tct aag cct gcg acc tgg ttc tgt gag	787	
Arg Ser Ile Asp Pro Thr Thr Ser Lys Pro Ala Thr Trp Phe Cys Glu		
215	220	225
ccc att ggg cac cgc caa gaa gac ggc gac tac gtg gaa tcc tgg cag	835	
Pro Ile Gly His Arg Gln Glu Asp Gly Asp Tyr Val Glu Ser Trp Gln		
230	235	240
cca atg gag atg act cct cgc gcg ctg gaa aac gca cgc tca gta gcc	883	
Pro Met Glu Met Thr Pro Arg Ala Leu Glu Asn Ala Arg Ser Val Ala		
250	255	260
gca cgc atc acc aac gca ttg ggc gga cgc ggc gta ttt ggt gtg gag	931	
Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly Val Phe Gly Val Glu		
265	270	275
ctc ttt gtc tcc ggc gat gac gtg tac ttc tct gaa gtc tcc cca cgc	979	
Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser Glu Val Ser Pro Arg		
280	285	290
cca cac gac acc ggc ctt gtc acc ctt gcc acc cag cgt ttc tct gaa		
1027		
Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr Gln Arg Phe Ser Glu		
295	300	305
ttt gaa ctc cac gcc aag gca att ctg gga ttg cct gtt gat gtc acc		
1075		
Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu Pro Val Asp Val Thr		
310	315	320
ctg att tct cca ggt gcc tcc gct gtc atc tac ggt ggc atc gaa tct		
1123		
Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr Gly Gly Ile Glu Ser		
330	335	340
gaa ggc gtg agc tac acc ggg ttg gct gaa gcg ctg gca gtg gct gaa		
1171		
Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala Leu Ala Val Ala Glu		
345	350	355
act gat ctt cgt atc ttt gcc aag cca gag gcc ttc acc aag cgt cgc		
1219		
Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala Phe Thr Lys Arg Arg		
360	365	370
atg ggt gtt gca gtg tcc acc gct gag gat gtg gct gca gcc agg gac		
1267		
Met Gly Val Ala Val Ser Thr Ala Glu Asp Val Ala Ala Ala Arg Asp		
375	380	385
cgc gcc act ttg gct gcc gcg gcg atc aag gtt cat cca gga aat tcc		
1315		
Arg Ala Thr Leu Ala Ala Ala Ala Ile Lys Val His Pro Gly Asn Ser		
390	395	400
		405

gca gag gct taacatgctg ggaaagcatc ggg  
 1347  
 Ala Glu Ala

<210> 910  
 <211> 408  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 910

Met	Tyr	Ile	Pro	Glu	Ser	Ile	Gly	Thr	Pro	Leu	Thr	Pro	Asn	Ala	Thr	1	5	10	15
Lys	Val	Met	Leu	Leu	Gly	Ser	Gly	Glu	Leu	Gly	Lys	Glu	Val	Ala	Ile	20	25	30	
Ala	Phe	Gln	Arg	Leu	Gly	Leu	Glu	Val	His	Ala	Val	Asp	Arg	Tyr	Glu	35	40	45	
His	Ala	Pro	Ala	His	Gln	Val	Ala	His	Phe	Ser	Tyr	Val	Ile	Asp	Met	50	55	60	
Thr	Asp	Ala	Ala	Gln	Val	Arg	Glu	Leu	Val	Glu	Arg	Val	Arg	Pro	Asp	65	70	75	80
Phe	Val	Ile	Pro	Glu	Ile	Glu	Ala	Leu	Ala	Thr	Asp	Glu	Leu	Val	Lys	85	90	95	
Ile	Glu	Glu	Glu	Gly	Leu	Ala	Thr	Ile	Val	Pro	Thr	Ala	Arg	Ala	Ala	100	105	110	
Lys	Leu	Thr	Met	Asn	Arg	Glu	Gly	Ile	Arg	Lys	Leu	Ala	Ala	Glu	Glu	115	120	125	
Leu	Gly	Leu	Pro	Thr	Ser	Asn	Tyr	Glu	Phe	Cys	Ser	Thr	Phe	Glu	Glu	130	135	140	
Phe	Ser	Ala	Ala	Ala	Glu	Lys	Leu	Gly	Tyr	Pro	Asn	Val	Val	Lys	Pro	145	150	155	160
Val	Met	Ser	Ser	Ser	Gly	Lys	Gly	Gln	Ser	Val	Leu	Arg	Ser	Ser	Asp	165	170	175	
Asp	Leu	Gln	Ala	Ala	Trp	Asp	Tyr	Ala	Met	Ser	Gly	Ala	Arg	Val	Ala	180	185	190	
Asn	Ser	Arg	Val	Ile	Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile	195	200	205	
Thr	Leu	Leu	Thr	Val	Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala	210	215	220	
Thr	Trp	Phe	Cys	Glu	Pro	Ile	Gly	His	Arg	Gln	Glu	Asp	Gly	Asp	Tyr	225	230	235	240
Val	Glu	Ser	Trp	Gln	Pro	Met	Glu	Met	Thr	Pro	Arg	Ala	Leu	Glu	Asn	245	250	255	



Ala Arg Ser Val Ala Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly  
 260 265 270

Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser  
 275 280 285

Glu Val Ser Pro Arg Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr  
 290 295 300

Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu  
 305 310 315 320

Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr  
 325 330 335

Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala  
 340 345 350

Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala  
 355 360 365

Phe Thr Lys Arg Arg Met Gly Val Ala Val Ser Thr Ala Glu Asp Val  
 370 375 380

Ala Ala Ala Arg Asp Arg Ala Thr Leu Ala Ala Ala Ala Ile Lys Val  
 385 390 395 400

His Pro Gly Asn Ser Ala Glu Ala  
 405

&lt;210&gt; 911

&lt;211&gt; 2409

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2386)

&lt;223&gt; RXN00537

&lt;400&gt; 911

accCGgaaca tgccgtcgaa aagctaaccg gcccattctat tgatggcctg gagctgttcc 60

tgtccgccgt tggcaccatc gcggttaag aggagtaaat atg agc act ttt gtc 115  
 Met Ser Thr Phe Val  
 1 5

aat gac acc gtc gaa gac gca atc aag acc cct gag ctg gat cag cca 163  
 Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro Glu Leu Asp Gln Pro  
 10 15 20

ttt gag gct ctt ggt ctg aaa gac gac gag tac gcg cgc atc aag gaa 211  
 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu  
 25 30 35

atc ctt ggc cgc cgc cca acc gac gcc gag ctg acc gtt tac tcc gtc 259  
 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val  
 40 45 50

atg tgg tcg gag cac tgc tcc tac aag tcc tcc aag gtt cac ctg cgt 307

Met	Trp	Ser	Glu	His	Cys	Ser	Tyr	Lys	Ser	Ser	Lys	Val	His	Leu	Arg	
55						60					65					
tac	ttc	ggt	gaa	acc	acc	act	gag	gaa	atg	gct	tcc	aag	att	ctt	gcc	355
Tyr	Phe	Gly	Glu	Thr	Thr	Thr	Glu	Glu	Met	Ala	Ser	Lys	Ile	Leu	Ala	
70					75				80						85	
ggc	atc	ggc	gag	aac	gct	ggt	gtg	gtc	gac	atc	gga	gac	ggc	aac	gcc	403
Gly	Ile	Gly	Glu	Asn	Ala	Gly	Val	Val	Asp	Ile	Gly	Asp	Gly	Asn	Ala	
				90					95					100		
gtg	acc	ttc	cgc	gtg	gag	tcc	cac	aac	cac	cca	tcc	ttc	gta	gag	cca	451
Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro	
			105					110					115			
cac	cag	ggc	gct	gcg	acc	ggc	gtc	ggc	ggc	atc	gtc	cgc	gac	att	atg	499
His	Gln	Gly	Ala	Ala	Thr	Gly	Val	Gly	Gly	Ile	Val	Arg	Asp	Ile	Met	
		120					125					130				
gct	atg	ggc	gca	cgc	cca	atc	gct	gtg	atg	gat	cag	ctg	cgt	ttc	ggt	547
Ala	Met	Gly	Ala	Arg	Pro	Ile	Ala	Val	Met	Asp	Gln	Leu	Arg	Phe	Gly	
	135					140				145						
gca	ctg	gac	aac	cca	gac	acc	cag	cgt	gtg	ttt	cct	ggc	gtt	gtt	gac	595
Ala	Leu	Asp	Asn	Pro	Asp	Thr	Gln	Arg	Val	Phe	Pro	Gly	Val	Val	Asp	
150					155				160						165	
ggc	att	tcc	cat	tac	ggc	aac	tgc	ctc	ggc	ctg	cca	aac	atc	ggt	ggc	643
Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu	Gly	Leu	Pro	Asn	Ile	Gly	Gly	
				170				175						180		
gaa	acc	gtc	ttc	gac	gat	tcc	tac	gca	ggt	aac	cca	ctg	gtc	aac	gca	691
Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn	Pro	Leu	Val	Asn	Ala	
			185					190					195			
ctg	tgc	gtg	ggt	acc	ctc	aag	gtg	gaa	gac	ctc	aag	ctt	gca	ttc	gca	739
Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu	Lys	Leu	Ala	Phe	Ala	
		200					205					210				
tcc	ggc	acc	ggc	aac	aag	gtg	atc	ctg	ttc	ggt	tcc	cgc	acc	ggc	ctt	787
Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly	Ser	Arg	Thr	Gly	Leu	
	215					220					225					
gat	ggc	atc	ggt	ggc	gtg	tcc	gtc	ctg	ggt	tcc	gca	tcc	ttc	gaa	gaa	835
Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser	Ala	Ser	Phe	Glu	Glu	
230					235				240						245	
ggc	gaa	gag	cgc	aag	ctc	cca	gct	gtt	cag	gtt	ggc	gat	cct	ttc	gca	883
Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val	Gly	Asp	Pro	Phe	Ala	
				250					255					260		
gag	aag	gta	ctc	atc	gag	tgc	tgc	ctc	gag	ctg	tac	aag	gct	ggc	gtc	931
Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu	Tyr	Lys	Ala	Gly	Val	
			265					270					275			
gtg	gtc	ggt	att	cag	gac	ctc	ggt	ggc	ggc	gga	ctt	gcg	tgt	gca	acc	979
Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly	Leu	Ala	Cys	Ala	Thr	
		280					285					290				
tct	gag	ctg	gca	gcc	gca	ggc	gac	ggc	ggc	atg	cgc	gtc	aac	cta	gac	1027

Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met Arg Val Asn Leu Asp  
 295 300 305  
 aac gtc cca ctg cgc gca gag aac atg tct gca gct gaa atc ctg gct  
 1075  
 Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala Ala Glu Ile Leu Ala  
 310 315 320 325  
 tcc gag tcc cag gag cgc atg tgt gct gtt gtc acc cct gaa aac gtt  
 1123  
 Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val Thr Pro Glu Asn Val  
 330 335 340  
 gag cgt ttc ctc gag atc tgt gca aag tgg gat gtc acc tgc gca gaa  
 1171  
 Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp Val Thr Cys Ala Glu  
 345 350 355  
 atc ggc gaa gtt acc gac gag aag gac cgc tac gtt gtg gtc cac aac  
 1219  
 Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr Val Val Val His Asn  
 360 365 370  
 ggt gaa gtt gtt atc gac gca cct cca tca acc atc gat gaa ggc cct  
 1267  
 Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr Ile Asp Glu Gly Pro  
 375 380 385  
 gtc tac aac cgc cca gtt gct cgc cct gag aac cag gac gaa ctg cag  
 1315  
 Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn Gln Asp Glu Leu Gln  
 390 395 400 405  
 ctc gaa ggc gag atc gct cgc cca gtc gac gtt gaa gag atc aag gct  
 1363  
 Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val Glu Glu Ile Lys Ala  
 410 415 420  
 gct tgg ctg aag ctt gtc gct tca cca gca ctt gca tcc cgc gcg ttt  
 1411  
 Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu Ala Ser Arg Ala Phe  
 425 430 435  
 atc acc gag cag tac gac cgc tac gtc cgc ggc aac acc gtt cag gca  
 1459  
 Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly Asn Thr Val Gln Ala  
 440 445 450  
 aag aac gcc aat gct ggc gtc ttg cgt atc gac gaa gag acc aac cgt  
 1507  
 Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr Asn Arg  
 455 460 465  
 ggc gtt gcg atc tcc gcc gac gca tcc ggc cgt tac acc aag ctc gag  
 1555  
 Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys Leu Glu  
 470 475 480 485  
 cca aac act ggc gcg cag ctt gca ctg gct gag gct tac cgc aac gtg  
 1603  
 Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg Asn Val

490										495					500					
gtc tcc acc ggt gca cgc cca gtg gct gtc acc aac tgc ctg aac ttc																				
1651																				
Val	Ser	Thr	Gly	Ala	Arg	Pro	Val	Ala	Val	Thr	Asn	Cys	Leu	Asn	Phe					
			505					510					515							
ggt tcc cca gaa aac gct ggt gtt atg tgg cag ttc aag gaa gca gtc																				
1699																				
Gly	Ser	Pro	Glu	Asn	Ala	Gly	Val	Met	Trp	Gln	Phe	Lys	Glu	Ala	Val					
		520					525					530								
cac ggt ctg gca gac gga tcc aag ctt ttg ggc att cca gtg tcc ggc																				
1747																				
His	Gly	Leu	Ala	Asp	Gly	Ser	Lys	Leu	Leu	Gly	Ile	Pro	Val	Ser	Gly					
	535					540					545									
ggt aac gtc tcc ttc tac aac cag act ggt gac gag ccc atc ctg cca																				
1795																				
Gly	Asn	Val	Ser	Phe	Tyr	Asn	Gln	Thr	Gly	Asp	Glu	Pro	Ile	Leu	Pro					
550					555					560					565					
acc cca gtc gtg ggt gtt ttg gga gtc ttg gac aac gtc gag cag agc																				
1843																				
Thr	Pro	Val	Val	Gly	Val	Leu	Gly	Val	Leu	Asp	Asn	Val	Glu	Gln	Ser					
				570					575						580					
atc ggc aac gtc ctc cca tcc gag gac aac gat ctc tac ctc ctg ggt																				
1891																				
Ile	Gly	Asn	Val	Leu	Pro	Ser	Glu	Asp	Asn	Asp	Leu	Tyr	Leu	Leu	Gly					
		585						590					595							
gag acc ttc gat gag ttc ggt ggc tcc atc tgg cag cag gtt tct ggc																				
1939																				
Glu	Thr	Phe	Asp	Glu	Phe	Gly	Gly	Ser	Ile	Trp	Gln	Gln	Val	Ser	Gly					
		600					605					610								
gct ggc ctc aac ggt ctg cca cca gta gtt gac ctg ctc aac gag cag																				
1987																				
Ala	Gly	Leu	Asn	Gly	Leu	Pro	Pro	Val	Val	Asp	Leu	Leu	Asn	Glu	Gln					
	615					620					625									
cgt ctt gca gac ctg ttc gtc ggt tct gat ctg ttt gct gca tcc cac																				
2035																				
Arg	Leu	Ala	Asp	Leu	Phe	Val	Gly	Ser	Asp	Leu	Phe	Ala	Ala	Ser	His					
630				635						640					645					
gat ctg tct gag ggc ggc ctt ggc cag acc ctc gca gag ctt gcg atc																				
2083																				
Asp	Leu	Ser	Glu	Gly	Gly	Leu	Gly	Gln	Thr	Leu	Ala	Glu	Leu	Ala	Ile					
			650						655					660						
cac cag aaa aag gga atg gat gtt gat ctc tcc cag atc cac cca tcc																				
2131																				
His	Gln	Lys	Lys	Gly	Met	Asp	Val	Asp	Leu	Ser	Gln	Ile	His	Pro	Ser					
			665					670					675							
ctg ttc acc tca ctg ttt gct gag tcc gct tcc cgc atc gtg gtt gca																				
2179																				
Leu	Phe	Thr	Ser	Leu	Phe	Ala	Glu	Ser	Ala	Ser	Arg	Ile	Val	Val	Ala					
			680				685						690							

acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt  
2227

Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val  
695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc  
2275

Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val  
710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa  
2323

Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu  
730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct  
2371

Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala  
745 750 755

aac gca gta gtt gca taattttctg ctgtgaagcc ggg  
2409

Asn Ala Val Val Ala  
760

<210> 912

<211> 762

<212> PRT

<213> Corynebacterium glutamicum

<400> 912

Met Ser Thr Phe Val Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro  
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Glu Leu Asp Gln Pro Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr  
20 25 30

Ala Arg Ile Lys Glu Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu  
35 40 45

Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser  
50 55 60

Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala  
65 70 75 80

Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile  
85 90 95

Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro  
100 105 110

Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile  
115 120 125

Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp  
130 135 140

Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe

145	150	155	160
Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu	165	170	175
Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn	180	185	190
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu	195	200	205
Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly	210	215	220
Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser	225	230	235
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val	245	250	255
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu	260	265	270
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly	275	280	285
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met	290	295	300
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala	305	310	315
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val	325	330	335
Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp	340	345	350
Val Thr Cys Ala Glu Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr	355	360	365
Val Val Val His Asn Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr	370	375	380
Ile Asp Glu Gly Pro Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn	385	390	395
Gln Asp Glu Leu Gln Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val	405	410	415
Glu Glu Ile Lys Ala Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu	420	425	430
Ala Ser Arg Ala Phe Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly	435	440	445
Asn Thr Val Gln Ala Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp	450	455	460
Glu Glu Thr Asn Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg	465	470	475
			480

Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu  
 485 490 495  
 Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr  
 500 505 510  
 Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln  
 515 520 525  
 Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly  
 530 535 540  
 Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp  
 545 550 555 560  
 Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp  
 565 570 575  
 Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp  
 580 585 590  
 Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp  
 595 600 605  
 Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp  
 610 615 620  
 Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu  
 625 630 635 640  
 Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu  
 645 650 655  
 Ala Glu Leu Ala Ile His Gln Lys Lys Gly Met Asp Val Asp Leu Ser  
 660 665 670  
 Gln Ile His Pro Ser Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser  
 675 680 685  
 Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala  
 690 695 700  
 Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser  
 705 710 715 720  
 Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val  
 725 730 735  
 Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly  
 740 745 750  
 His Ala Val Gly Ala Asn Ala Val Val Ala  
 755 760

&lt;210&gt; 913

&lt;211&gt; 638

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (54)..(638)

&lt;223&gt; FRXA02805

&lt;400&gt; 913

tgtgatggat cagctgcgtt tcgggtgcac tggacaaccc agacaccag cgtgtg ttt 59

Val Phe

1

cct ggc gtt gtt gac ggc att tcc cat tac ggc aac tgc ctc ggc ctg 107

Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu

5

10

15

cca aac atc ggt ggc gaa acc gtc ttc gac gat tcc tac gca ggt aac 155

Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn

20

25

30

cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203

Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu

35

40

45

50

aag ctt gca ttc gca tcc ggc acc ggc aac aag gtg atc ctg ttc ggt 251

Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly

55

60

65

tcc cgc acc ggc ctt gat ggc atc ggt ggc gtg tcc gtc ctg ggt tcc 299

Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser

70

75

80

gca tcc ttc gaa gaa ggc gaa gag cgc aag ctc cca gct gtt cag gtt 347

Ala Ser Phe Glu Glu Gly Glu Arg Lys Leu Pro Ala Val Gln Val

85

90

95

ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395

Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu

100

105

110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443

Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly

115

120

125

130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491

Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met

135

140

145

cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539

Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala

150

155

160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587

Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val

165

170

175

acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635

Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp

180

185

190

gtc

Val

195

638



<210> 914  
 <211> 195  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 914

Val Phe Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu  
 1 5 10 15  
 Gly Leu Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala  
 20 25 30  
 Gly Asn Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu  
 35 40 45  
 Asp Leu Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu  
 50 55 60  
 Phe Gly Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu  
 65 70 75 80  
 Gly Ser Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val  
 85 90 95  
 Gln Val Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu  
 100 105 110  
 Glu Leu Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly  
 115 120 125  
 Gly Gly Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly  
 130 135 140  
 Gly Met Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met  
 145 150 155 160  
 Ser Ala Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala  
 165 170 175  
 Val Val Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys  
 180 185 190  
 Trp Asp Val  
 195

<210> 915  
 <211> 697  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (23) .. (697)  
 <223> FRXA00537

<400> 915

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 Val Tyr His Arg Ala Val Leu Asn Ala Thr

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tcc gcg gca aca ccg ttc aag caa aag aac gcc aat gct ggc gtc ttg				100
Ser Ala Ala Thr Pro Phe Lys Gln Lys Asn Ala Asn Ala Gly Val Leu	15	20	25	
cgt atc gac gaa gag acc anc cgt ggc gtt gcg atc tcc gcc gac gca				148
Arg Ile Asp Glu Glu Thr Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala	30	35	40	
tcc ggc cgt tac acc aag ctc gag cca aac act ggc gcg cag ctt gca				196
Ser Gly Arg Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala	45	50	55	
ctg gct gag gct tac cgc aac gtg gtc tcc acc ggt gca cgc cca gtg				244
Leu Ala Glu Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val	60	65	70	
gct gtc acc aac tgc ctg aac ttc ggt tcc cca gaa aac gct ggt gtt				292
Ala Val Thr Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val	75	80	85	90
atg tgg cag ttc aag gaa gca gtc cac ggt ctg gca gac gga tcc aag				340
Met Trp Gln Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys	95	100	105	
ctt ttg ggc att cca gtg tcc ggc ggt aac gtc tcc ttc tac aac cag				388
Leu Leu Gly Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln	110	115	120	
act ggt gac gag ccc atc ctg cca acc cca gtc gtg ggt gtt ttg gga				436
Thr Gly Asp Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly	125	130	135	
gtc ttg gac aac gtc gag cag agc atc ggc aac gtc ctc cca tcc gag				484
Val Leu Asp Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu	140	145	150	
gac aac gat ctc tac ctc ctg ggt gag acc ttc gat gag ttc ggt ggc				532
Asp Asn Asp Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly	155	160	165	170
tcc atc tgg cag cag gtt tct ggc gct ggc ctc aac ggt ctg cca cca				580
Ser Ile Trp Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro	175	180	185	
gta gtt gac ctg ctc aac gag cag cgt ctt gca gac ctg ttc gtc ggt				628
Val Val Asp Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly	190	195	200	
tct gat ctg ttt gct gca tcc cac gat ctg tct gag ggc ggc ctt ggc				676
Ser Asp Leu Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly	205	210	215	
cag acc ctc gca gag ctt gcg				697
Gln Thr Leu Ala Glu Leu Ala	220	225		

&lt;210&gt; 916

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 916

Val Tyr His Arg Ala Val Leu Asn Ala Thr Ser Ala Ala Thr Pro Phe  
 1 5 10 15

Lys Gln Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr  
 20 25 30

Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys  
 35 40 45

Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg  
 50 55 60

Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu  
 65 70 75 80

Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu  
 85 90 95

Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val  
 100 105 110

Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile  
 115 120 125

Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu  
 130 135 140

Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu  
 145 150 155 160

Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val  
 165 170 175

Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn  
 180 185 190

Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala  
 195 200 205

Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu  
 210 215 220

Ala

225

&lt;210&gt; 917

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (279)

&lt;223&gt; FRXA00561

&lt;400&gt; 917

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ctc ttc cca gat cca ccc atc cct gtt cac ctc act tgt ttg ctg agt 48
Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser
  1              5              10              15

ccc gct tcc cgc atc gtg gtt gca acc aac cgc ggc gaa gag ttg gaa 96
Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
          20              25              30

aag cgc gca gca gag ctg ggt gtt cca gtg ttc aag ctg ggc tgc acc 144
Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
          35              40              45

aac gat tca gcc gtc atc gct gtc aag ggc gca gac gtt gag ttc act 192
Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
          50              55              60

gtt tcc gtg gag gaa ctc cgc gaa gca tgg acc aac act ttg cct gag 240
Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
  65              70              75              80

gcc ttc ggt cac gca gtt gga gct aac gca gta gtt gca taattttctg 289
Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
          85              90

ctgtgaagcc ggg 302

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<210> 918  
 <211> 93  
 <212> PRT  
 <213> Corynebacterium glutamicum

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<400> 918
Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser
  1              5              10              15

Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
          20              25              30

Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
          35              40              45

Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
          50              55              60

Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
  65              70              75              80

Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
          85              90

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<210> 919  
 <211> 792  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(769)  
 <223> RXA00541

&lt;400&gt; 919

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tcatcgaaga cttcgatgtg gtgggagttg aggtcgcgaa gtg agc gcc aaa atc 115  
Val Ser Ala Lys Ile  
1 5

ggg gtc att acc ttc cca ggc acc ctt gac gat gta gat gca gca cgc 163  
Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp Val Asp Ala Ala Arg  
10 15 20

gct gct cgc atc gca ggt gca gaa gta atc agc ctg tgg cac gct gac 211  
Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser Leu Trp His Ala Asp  
25 30 35

gag gat ctc aag ggc gtc gac gca gtt gtc gtt ccc ggt gga ttc tcc 259  
Glu Asp Leu Lys Gly Val Asp Ala Val Val Val Pro Gly Gly Phe Ser  
40 45 50

tac ggc gat tac ctg cgc acc ggt gca atc tct gca ctg gcg cca gta 307  
Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser Ala Leu Ala Pro Val  
55 60 65

atg cag tcc gtg att gag cag gcc ggt aag ggt atg cca gtc ttg ggc 355  
Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly Met Pro Val Leu Gly  
70 75 80 85

att tgc aac ggc ttc cag atc ctc acc gaa gca cgc ctg ctt cca ggc 403  
Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala Arg Leu Leu Pro Gly  
90 95 100

gcg ctg acc cgc aac aag ggt ctg cac ttt cac tgt gta gac gca cac 451  
Ala Leu Thr Arg Asn Lys Gly Leu His Phe His Cys Val Asp Ala His  
105 110 115

ctc gtt gta gag aac aac acc act gca tgg acc aac act ttg gaa aag 499  
Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr Asn Thr Leu Glu Lys  
120 125 130

ggg cag cag atc ctt att cct gca aag cac ggt gaa ggt cgc ttc cag 547  
Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly Glu Gly Arg Phe Gln  
135 140 145

gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg 595  
Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val  
150 155 160 165

ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt 643  
Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly  
170 175 180

atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa 691  
Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu  
185 190 195

cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg 739  
His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu  
200 205 210

ttc ctg tcc gcc gtt ggc acc atc gcg gct taagaggagt aaatatgagc 789

Phe Leu Ser Ala Val Gly Thr Ile Ala Ala  
215 220

act

792

<210> 920  
<211> 223  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 920

Val Ser Ala Lys Ile Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp  
1 5 10 15

Val Asp Ala Ala Arg Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser  
20 25 30

Leu Trp His Ala Asp Glu Asp Leu Lys Gly Val Asp Ala Val Val Val  
35 40 45

Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser  
50 55 60

Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly  
65 70 75 80

Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala  
85 90 95

Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His  
100 105 110

Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr  
115 120 125

Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly  
130 135 140

Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly  
145 150 155 160

Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val  
165 170 175

Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu  
180 185 190

Met Pro His Pro Glu His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile  
195 200 205

Asp Gly Leu Glu Leu Phe Leu Ser Ala Val Gly Thr Ile Ala Ala  
210 215 220

<210> 921  
<211> 1014  
<212> DNA  
<213> Corynebacterium glutamicum

<220>

<221> CDS  
 <222> (101)..(991)  
 <223> RXA00620

<400> 921

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aattttccga acacacccga ggggtctaga cttgcctaac atg cgt cct gaa ctc 115
                                         Met Arg Pro Glu Leu
                                         1           5

tcc cag tac aag cac ctg tcg gca ggc aag gtc cgt gag atc tac gag 163
Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu
                10                15                20

atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211
Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala
                25                30                35

tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259
Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu
                40                45                50

act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307
Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His
                55                60                65

ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355
Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly
                70                75                80                85

cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403
Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val
                90                95                100

gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451
Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr
                105                110                115

agc tcc gtg tgt gga gtt gag ctc cca gaa ggc ctc gtt gaa tct tct 499
Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser
                120                125                130

cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547
Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly
                135                140                145

gac cac gac atc aat gtc tcc ttt gac gtt gtt gaa gaa cgt ctc ggc 595
Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly
                150                155                160                165

gaa gct cgt gcg aac cag ttg cgc gat gcc tct att gct att tac aag 643
Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys
                170                175                180

gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691
Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val Ile Leu Ala Asp Thr
                185                190                195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739
Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp

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200	205	210	
gaa gtc ctt acc cca gat tcc tcc cgc tac tgg cct ttg gaa ggc tat			787
Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp Pro Leu Glu Gly Tyr			
215	220	225	
gaa gca gga tct gtg caa cca agc ttt gat aag caa ttc gtg cgc aac			835
Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn			
230	235	240	245
tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag			883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu			
250	255	260	
cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac			931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr			
265	270	275	
atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att			979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile			
280	285	290	

ggt tct tgc gtc taagctgctt gattttccct aaa  
 1014  
 Gly Ser Cys Val  
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 <213> Corynebacterium glutamicum

<400> 922  
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 Arg Glu Ile Tyr Glu Ile Asp Asp Lys His Ile Leu Met Val Ala Ser  
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 Asp Arg Ile Ser Ala Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp  
 35 40 45  
 Lys Gly Arg Val Leu Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile  
 50 55 60  
 Asp Phe Pro Asn His Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro  
 65 70 75 80  
 Glu Glu Val Leu Gly Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu  
 85 90 95  
 Pro Phe Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val  
 100 105 110  
 Glu Tyr Lys Gln Thr Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly  
 115 120 125  
 Leu Val Glu Ser Ser Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr  
 130 135 140



Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val  
 145 150 155 160  
 Glu Glu Arg Leu Gly Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser  
 165 170 175  
 Ile Ala Ile Tyr Lys Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val  
 180 185 190  
 Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr  
 195 200 205  
 Leu Val Leu Gly Asp Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp  
 210 215 220  
 Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys  
 225 230 235 240  
 Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys  
 245 250 255  
 Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala  
 260 265 270  
 Thr Arg Glu Arg Tyr Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys  
 275 280 285  
 Phe Cys Gln Trp Ile Gly Ser Cys Val  
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&lt;210&gt; 923

&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1270)

&lt;223&gt; RXN00770

&lt;400&gt; 923

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 cctcaagtta agatcggtag gcgatagggg ttgagcattt ttg ctc tcc ccg tat 115  
 Leu Leu Ser Pro Tyr  
 1 5  
 gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163  
 Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys  
 10 15 20  
 ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211  
 Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln  
 25 30 35  
 gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259  
 Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile  
 40 45 50  
 gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307

Glu	Ala	Gly	Asp	Arg	Ala	Val	Glu	Leu	Phe	Ala	Pro	Met	Ala	Lys	Arg		
55						60					65						
gcc	acc	cgc	cca	gag	gtt	ctt	ggc	aac	ctc	gga	ggc	ttc	gca	gga	ctc	355	
Ala	Thr	Arg	Pro	Glu	Val	Leu	Gly	Asn	Leu	Gly	Gly	Phe	Ala	Gly	Leu		
70					75					80					85		
ttt	gag	ctc	gga	aaa	tac	aag	aag	cca	atc	ctc	gca	gca	gga	tct	gac	403	
Phe	Glu	Leu	Gly	Lys	Tyr	Lys	Lys	Pro	Ile	Leu	Ala	Ala	Gly	Ser	Asp		
				90					95					100			
gga	gtc	ggc	acc	aag	ctt	gtc	atc	gcc	cag	atg	atg	gac	aag	cac	gac	451	
Gly	Val	Gly	Thr	Lys	Leu	Val	Ile	Ala	Gln	Met	Met	Asp	Lys	His	Asp		
			105					110					115				
acc	atc	ggc	atc	gac	ctt	gtt	gca	atg	tgt	gtg	gat	gac	ctc	gtt	gtc	499	
Thr	Ile	Gly	Ile	Asp	Leu	Val	Ala	Met	Cys	Val	Asp	Asp	Leu	Val	Val		
		120					125					130					
acc	ggc	gca	gag	cca	ctg	ttc	ctc	cag	gac	tac	atc	gcc	atc	ggc	aag	547	
Thr	Gly	Ala	Glu	Pro	Leu	Phe	Leu	Gln	Asp	Tyr	Ile	Ala	Ile	Gly	Lys		
	135				140						145						
gtt	gtc	cca	gag	cac	gtt	gct	gag	atc	gtc	tcc	ggg	atc	gca	gaa	ggc	595	
Val	Val	Pro	Glu	His	Val	Ala	Glu	Ile	Val	Ser	Gly	Ile	Ala	Glu	Gly		
150					155					160					165		
tgt	gtc	cag	gca	ggc	tgt	gct	ctg	ctc	ggg	ggc	gaa	acc	gca	gaa	cac	643	
Cys	Val	Gln	Ala	Gly	Cys	Ala	Leu	Leu	Gly	Gly	Glu	Thr	Ala	Glu	His		
				170					175					180			
cca	ggg	gtt	atg	gaa	cca	gac	cac	tac	gat	gtc	tcc	gca	act	gca	gtc	691	
Pro	Gly	Val	Met	Glu	Pro	Asp	His	Tyr	Asp	Val	Ser	Ala	Thr	Ala	Val		
			185					190					195				
ggc	gtt	gtc	gaa	gca	gat	gaa	ctg	cta	gga	cca	gac	cgc	gtc	cgc	gca	739	
Gly	Val	Val	Glu	Ala	Asp	Glu	Leu	Leu	Gly	Pro	Asp	Arg	Val	Arg	Ala		
		200				205						210					
ggc	gac	gtc	ctc	atc	ggc	atg	gct	tcc	tcc	ggg	ctg	cac	tcc	aac	ggg	787	
Gly	Asp	Val	Leu	Ile	Gly	Met	Ala	Ser	Ser	Gly	Leu	His	Ser	Asn	Gly		
	215				220					225							
tac	tcc	ctg	gct	cgc	cac	gtc	ctc	ctg	gaa	aag	gca	ggc	ctg	gcg	ctt	835	
Tyr	Ser	Leu	Ala	Arg	His	Val	Leu	Leu	Glu	Lys	Ala	Gly	Leu	Ala	Leu		
230					235					240					245		
gac	gga	cac	atc	gaa	gaa	ctc	gga	cgc	acc	ctc	ggg	gaa	gaa	ctt	ctc	883	
Asp	Gly	His	Ile	Glu	Glu	Leu	Gly	Arg	Thr	Leu	Gly	Glu	Glu	Leu	Leu		
				250				255						260			
gag	cca	acc	cgc	atc	tac	gcc	aag	gac	tgc	ctg	gca	ctg	atc	gca	gag	931	
Glu	Pro	Thr	Arg	Ile	Tyr	Ala	Lys	Asp	Cys	Leu	Ala	Leu	Ile	Ala	Glu		
			265					270					275				
tgc	gaa	gtt	cac	acc	ttc	tgc	cac	gtc	acc	ggc	ggc	ggc	ctc	gca	ggc	979	
Cys	Glu	Val	His	Thr	Phe	Cys	His	Val	Thr	Gly	Gly	Gly	Leu	Ala	Gly		
		280				285						290					
aac	ctc	gag	cgg	gtt	gtc	cca	gaa	ggg	ctc	gtc	gca	gaa	atg	tcc	cga	1027	

Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val Ala Glu Met Ser Arg  
 295 300 305  
 gca act tgg acc cca ggc caa atc ttc cgc acc atc tcc tct gtg ggc  
 1075  
 Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly  
 310 315 320 325  
 aag gtt tcc cgc gaa gaa atg gaa aag acc ttc aac atg ggt gtc ggc  
 1123  
 Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly  
 330 335 340  
 atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg  
 1171  
 Met Val Ala Val Val Ala Glu Lys Asp Arg Asp Arg Ala Leu Ala Met  
 345 350 355  
 ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac  
 1219  
 Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn  
 360 365 370  
 ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc  
 1267  
 Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn Gly Glu His Pro Gly  
 375 380 385  
 tac taagcccaac tgtctgctct aag  
 1293  
 Tyr  
 390  
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 20 25 30  
 Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala  
 35 40 45  
 Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala  
 50 55 60  
 Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly  
 65 70 75 80  
 Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu  
 85 90 95  
 Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met  
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val  
 115 120 125  
 Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr  
 130 135 140  
 Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser  
 145 150 155 160  
 Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly  
 165 170 175  
 Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val  
 180 185 190  
 Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro  
 195 200 205  
 Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly  
 210 215 220  
 Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys  
 225 230 235 240  
 Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu  
 245 250 255  
 Gly Glu Glu Leu Leu Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu  
 260 265 270  
 Ala Leu Ile Ala Glu Cys Glu Val His Thr Phe Cys His Val Thr Gly  
 275 280 285  
 Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val  
 290 295 300  
 Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr  
 305 310 315 320  
 Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe  
 325 330 335  
 Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys Asp Arg Asp  
 340 345 350  
 Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile  
 355 360 365  
 Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn  
 370 375 380  
 Gly Glu His Pro Gly Tyr  
 385 390

&lt;210&gt; 925

&lt;211&gt; 818

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (15)..(818)

&lt;223&gt; FRXA00557

&lt;400&gt; 925

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Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala	
1 5 10	
ctt tta gac agt tat gtt cct aat aag ttc caa acc cca gca gga gaa	98
Leu Leu Asp Ser Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu	
15 20 25	
gcg aag tac acg atg agt gat cac cag gac acc acc gcc gaa ggc gtt	146
Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val	
30 35 40	
tca tac gca gca gca gga gtc gac atc gaa gcc ggc gat cgt gcc gtc	194
Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val	
45 50 55 60	
gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt	242
Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu	
65 70 75	
ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag	290
Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys	
80 85 90	
aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc	338
Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val	
95 100 105	
atc gcc cag atg atg gac aag cac gac acc atc ggc atc gac ctt gtt	386
Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val	
110 115 120	
gca atg tgt gtg gat gac ctc gtt gtc acc ggc gca gag cca ctg ttc	434
Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe	
125 130 135 140	
ctc cag gac tac atc gcc atc ggc aag gtt gtc cca gag cac gtt gct	482
Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala	
145 150 155	
gag atc gtc tcc ggt atc gca gaa ggc tgt gtc cag gca ggc tgt gct	530
Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala	
160 165 170	
ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac	578
Leu Leu Gly Gly Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp	
175 180 185	
cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa	626
His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu	
190 195 200	
ctg cta gga cca gac cgc gtc cgc gca ggc gac gtc ctc atc ggc atg	674
Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met	
205 210 215 220	

gct tcc tcc ggt ctg cac tcc aac ggt tac tcc ctg gct cgc cac gtc 722  
 Ala Ser Ser Gly Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val  
                   225                                  230                                  235

ctc ctg gaa aag gca ggc ctg gcg ctt gac gga cac atc gaa gaa ctc 770  
 Leu Leu Glu Lys Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu  
                   240                                  245                                  250

gga cgc acc ccc ggt gaa gaa ctt ctc gag cca acc cgc atg tac gcc 818  
 Gly Arg Thr Pro Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala  
                   255                                  260                                  265

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<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 926

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Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr  
                   20                                  25                                  30

Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala  
                   35                                  40                                  45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala  
   50                                  55                                  60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly  
   65                                  70                                  75                                  80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu  
                   85                                  90                                  95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met  
                   100                                  105                                  110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val  
                   115                                  120                                  125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr  
   130                                  135                                  140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser  
   145                                  150                                  155                                  160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly  
                   165                                  170                                  175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val  
                   180                                  185                                  190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro  
                   195                                  200                                  205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly  
   210                                  215                                  220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys  
 225 230 235 240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Pro  
 245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala  
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<210> 927

<211> 338

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(315)

<223> FRXA00770

<400> 927

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ggg ctc gtc gca gaa atg tcc cga gca act tgg acc cca ggc caa atc 96  
 Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile  
 20 25 30

ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa 144  
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu  
 35 40 45

aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag 192  
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys  
 50 55 60

gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc 240  
 Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys  
 65 70 75 80

tgg gaa atc gga acc gta cgc aac ggt gaa gag gga gag cct cgc gtg 288  
 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val  
 85 90 95

atc ctc aac ggc gag cac cct ggc tac taagcccaac tgtctgtctct 335  
 Ile Leu Asn Gly Glu His Pro Gly Tyr  
 100 105

aag 338

<210> 928

<211> 105

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 928

Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu  
 1 5 10 15

Gly	Leu	Val	Ala	Glu	Met	Ser	Arg	Ala	Thr	Trp	Thr	Pro	Gly	Gln	Ile
			20					25					30		
Phe	Arg	Thr	Ile	Ser	Ser	Val	Gly	Lys	Val	Ser	Arg	Glu	Glu	Met	Glu
		35					40					45			
Lys	Thr	Phe	Asn	Met	Gly	Val	Gly	Met	Val	Ala	Val	Val	Ala	Glu	Lys
	50					55					60				
Asp	Arg	Asp	Arg	Ala	Leu	Ala	Met	Leu	Thr	Ala	Arg	His	Ile	Asp	Cys
65					70					75					80
Trp	Glu	Ile	Gly	Thr	Val	Arg	Asn	Gly	Glu	Glu	Gly	Glu	Pro	Arg	Val
				85					90					95	
Ile	Leu	Asn	Gly	Glu	His	Pro	Gly	Tyr							
			100					105							

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<211> 1320
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1297)
<223> RXN02345
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				Val	Thr	Ser	Thr	Gly	5							
				1												
aac	caa	gcc	cac	gct	cca	gga	atg	ccc	atc	gtc	gca	gta	att	ggg	gac	163
Asn	Gln	Ala	His	Ala	Pro	Gly	Met	Pro	Ile	Val	Ala	Val	Ile	Gly	Asp	
				10				15						20		
ggc	caa	tta	gcc	cgc	atg	atg	cag	acc	tcc	gcc	atc	gaa	ctc	gga	caa	211
Gly	Gln	Leu	Ala	Arg	Met	Met	Gln	Thr	Ser	Ala	Ile	Glu	Leu	Gly	Gln	
			25				30						35			
tca	ctg	cga	gtt	cta	gct	gga	gcg	ccg	gat	tcc	tcc	gca	gct	caa	gta	259
Ser	Leu	Arg	Val	Leu	Ala	Gly	Ala	Pro	Asp	Ser	Ser	Ala	Ala	Gln	Val	
		40				45						50				
gct	gct	gat	gtt	gtt	ctc	ggc	gat	tac	acc	aac	att	gat	gat	ctg	cgc	307
Ala	Ala	Asp	Val	Val	Leu	Gly	Asp	Tyr	Thr	Asn	Ile	Asp	Asp	Leu	Arg	
		55				60					65					
gtc	gcc	atc	gaa	ggc	gcc	gat	gtg	atg	acc	ttc	gac	cac	gag	cac	gtc	355
Val	Ala	Ile	Glu	Gly	Ala	Asp	Val	Met	Thr	Phe	Asp	His	Glu	His	Val	
	70				75				80						85	
ccc	aac	gaa	cac	ctg	cac	caa	ctc	atc	gca	gaa	ggc	gtc	aac	gtt	cag	403
Pro	Asn	Glu	His	Leu	His	Gln	Leu	Ile	Ala	Glu	Gly	Val	Asn	Val	Gln	
				90				95						100		
cca	cgc	cca	gaa	gcg	ctg	gtc	aac	gca	caa	gac	aaa	ctt	gtc	atg	cgc	451



Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp Lys Leu Val Met Arg	
105 110 115	
aag cgt cta cgt gaa ctc ggc gca cca gtc cca cca ttt gct gcc att	499
Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro Pro Phe Ala Ala Ile	
120 125 130	
gaa tca gtc gaa gat gca gtg gga ttc ttc gaa gca gtt gat ggc caa	547
Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala Val Asp Gly Gln	
135 140 145	
gtt tgc ctc aaa gca cgc cgt ggc gga tac gac ggc aag ggc gta tgg	595
Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly Lys Gly Val Trp	
150 155 160 165	
ttc cca gcc gat gta gca gag ctt cag tcg ctt gtg gca gag ctt ctc	643
Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val Ala Glu Leu Leu	
170 175 180	
gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt gcc ctc aac agg	691
Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val Ala Leu Asn Arg	
185 190 195	
gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga gaa acc aaa gcg	739
Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly Glu Thr Lys Ala	
200 205 210	
tgg cca gtc gta gaa tca gtg cag aag aac ggt gtg tgt gca gaa gca	787
Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val Cys Ala Glu Ala	
215 220 225	
atc gct ccc gca cct gaa cta tcc gca gaa ctg cag gaa tcc acc aga	835
Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln Glu Ser Thr Arg	
230 235 240 245	
gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc act ggt gtc ttg	883
Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val Thr Gly Val Leu	
250 255 260	
gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg cag cca gag atc	931
Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly Gln Pro Glu Ile	
265 270 275	
ttt gtc aac gag ctc gcc atg cgt tca cac aac acc ggc cac tgg act	979
Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr Gly His Trp Thr	
280 285 290	
caa gat ggc tgc gtg acc agc caa ttc gag cag cac ctc cgc gca gtc	
1027	
Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His Leu Arg Ala Val	
295 300 305	
ctc gac tac cca ctg ggt gct acc gac act ttg gct gat tac acc gtg	
1075	
Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala Asp Tyr Thr Val	
310 315 320 325	
atg gcc aac gtg ctc ggt gcc gac acc gac cca gag atg ccc atg gca	
1123	
Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu Met Pro Met Ala	
330 335 340	

acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac  
1171

Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His  
345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac  
1219

Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn  
360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc  
1267

Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys  
375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgcta  
1317

Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
390 395

gca  
1320

<210> 930

<211> 399

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 930

Val Thr Ser Thr Gly Asn Gln Ala His Ala Pro Gly Met Pro Ile Val  
1 5 10 15

Ala Val Ile Gly Asp Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala  
20 25 30

Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser  
35 40 45

Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn  
50 55 60

Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe  
65 70 75 80

Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu  
85 90 95

Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp  
100 105 110

Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro  
115 120 125

Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu  
130 135 140

Ala Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp  
145 150 155 160

Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu  
 165 170 175  
 Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys  
 180 185 190  
 Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser  
 195 200 205  
 Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly  
 210 215 220  
 Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu  
 225 230 235 240  
 Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly  
 245 250 255  
 Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn  
 260 265 270  
 Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn  
 275 280 285  
 Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln  
 290 295 300  
 His Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu  
 305 310 315 320  
 Ala Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro  
 325 330 335  
 Glu Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro  
 340 345 350  
 Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys  
 355 360 365  
 Ile Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala  
 370 375 380  
 Glu Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
 385 390 395

&lt;210&gt; 931

&lt;211&gt; 833

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(810)

&lt;223&gt; FRXA02345

&lt;400&gt; 931

ttt gct gcc att gaa tca gtc gaa gat gca gtg gga ttc ttc gaa gca 48  
 Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala  
 1 5 10 15

gtt gat ggc caa gtt tgc ctc aaa gca cgc cgt ggc gga tac gac ggc	96
Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly	
20 25 30	
aag ggc gta tgg ttc cca gcc gat gta gca gag ctt cag tgc ctt gtg	144
Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val	
35 40 45	
gca gag ctt ctc gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt	192
Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val	
50 55 60	
gcc ctc aac agg gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga	240
Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly	
65 70 75 80	
gaa acc aaa gcg tgg cca gtc gta gaa tca gtg cag aag aac ggt gtg	288
Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val	
85 90 95	
tgt gca gaa gca atc gct ccc gca cct gaa cta tcc gca gaa ctg cag	336
Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln	
100 105 110	
gaa tcc acc aga gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc	384
Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val	
115 120 125	
act ggt gtc ttg gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg	432
Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly	
130 135 140	
cag cca gag atc ttt gtc aac gag ctc gcc atg cgt tca cac aac acc	480
Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr	
145 150 155 160	
ggc cac tgg act caa gat ggc tgc gtg acc agc caa ttc gag cag cac	528
Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His	
165 170 175	
ctc cgc gca gtc ctc gac tac cca ctg ggt gct acc gac act ttg gct	576
Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala	
180 185 190	
gat tac acc gtg atg gcc aac gtg ctc ggt gcc gac acc gac cca gag	624
Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu	
195 200 205	
atg ccc atg gca acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat	672
Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp	
210 215 220	
gcc aag att cac ctc tac ggc aag gga cat cgc ccg gga cga aag att	720
Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile	
225 230 235 240	
ggc cac gtc aac atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa	768
Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu	
245 250 255	
gcc ctg gcc tgc gca tac ttc ctt gtc aac gct cgc tgg gat	810

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
 260 265 270

taggtctttt ctgagcgcta gca

833

<210> 932

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 932

Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala  
 1 5 10 15

Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly  
 20 25 30

Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val  
 35 40 45

Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val  
 50 55 60

Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly  
 65 70 75 80

Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val  
 85 90 95

Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln  
 100 105 110

Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val  
 115 120 125

Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly  
 130 135 140

Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr  
 145 150 155 160

Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His  
 165 170 175

Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala  
 180 185 190

Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu  
 195 200 205

Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp  
 210 215 220

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile  
 225 230 235 240

Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu  
 245 250 255

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp

260

265

270

&lt;210&gt; 933

&lt;211&gt; 618

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(595)

&lt;223&gt; RXN02350

&lt;400&gt; 933

aagcattttct ccaacactttt tgatggacag attaacgctt aaaaggcctg ttatagactg 60

ataaaccgat acgtactttt cgcgcttaag gagaatttca gtg ggt cct cta gtt 115  
 Val Gly Pro Leu Val  
 1 5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163  
 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala  
 10 15 20

gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211  
 Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val  
 25 30 35

tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca 259  
 Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala  
 40 45 50

cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca 307  
 His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala  
 55 60 65

cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt 355  
 His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly  
 70 75 80 85

ggt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc 403  
 Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser  
 90 95 100

atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt 451  
 Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly  
 105 110 115

ggc gcg aag aat gca ggc cta ctt gcc gtt cgt att ctc ggt gct ggt 499  
 Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly  
 120 125 130

gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg 547  
 Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala  
 135 140 145

aag gaa gtt gaa gcc aag gac gaa gca ctg aag aag cgc ttg ctc ggc 595  
 Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly  
 150 155 160 165

taatgaatcc gatcgtggtg ctg 618

<210> 934  
 <211> 165  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 934

Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp  
 1 5 10 15  
 Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe  
 20 25 30  
 Glu Val Gly Val Val Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn  
 35 40 45  
 Tyr Ala Lys Thr Ala His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys  
 50 55 60  
 Ala Gly Gly Ala Ala His Leu Pro Gly Met Val Ala Ala Ala Thr Pro  
 65 70 75 80  
 Leu Pro Val Ile Gly Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu  
 85 90 95  
 Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val Ala  
 100 105 110  
 Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg  
 115 120 125  
 Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr  
 130 135 140  
 Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys  
 145 150 155 160  
 Lys Arg Leu Leu Gly  
 165

<210> 935  
 <211> 223  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(223)  
 <223> FRXA02346

<400> 935

aagcatttct ccaacacttt tgatggacag attaacgctt aaaaggcctg ttatagactg 60  
 ataaaccgat acgtaacttt cgcgcttaag gagaatttca gtg ggt cct cta gtt 115  
 Val Gly Pro Leu Val  
 1 5  
 ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163  
 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala

	10	15	20	
gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc				211
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val				
	25	30	35	
tct gca cac cgc				223
Ser Ala His Arg				
	40			
<210> 936				
<211> 41				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 936				
Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp				
1	5	10	15	
Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe				
	20	25	30	
Glu Val Gly Val Val Ser Ala His Arg				
	35	40		
<210> 937				
<211> 252				
<212> DNA				
<213> Corynebacterium glutamicum				
<220>				
<221> CDS				
<222> (20)..(229)				
<223> FRXA02350				
<400> 937				
atactaggat ctgcacgggtttg gat tcc ttg ctg tcc atc gtc cag atg cca				52
	Leu Asp Ser Leu Leu Ser Ile Val Gln Met Pro			
	1	5	10	
ggc ggc gtt cca gtc gcc act gtc tcc atc ggt ggc gcg aag aat gca				100
Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala				
	15	20	25	
ggc cta ctt gcc gtt cgt att ctc ggt gct ggt gat cct tct ttg gtc				148
Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val				
	30	35	40	
acg aag atg gcc gat tac caa gag aat atg gcg aag gaa gtt gaa gcc				196
Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala				
	45	50	55	
aag gac gaa gca ctg aag aag cgc ttg ctc ggc taatgaatcc gatcgtggtg				249
Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly				
	60	65	70	
ctg				252



<210> 938  
 <211> 70  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 938  
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           1                  5                  10                  15  
 Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val  
                   20                  25                  30  
 Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp  
           35                  40                  45  
 Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu  
           50                  55                  60  
 Lys Lys Arg Leu Leu Gly  
           65                  70

<210> 939  
 <211> 999  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(976)  
 <223> RXA01087

<400> 939  
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 tatctctaata ccaaactgca cctatatata aggagtaaaa atg caa acc ctt gct 115  
   Met Gln Thr Leu Ala  
   1                  5  
 gct att gtt cgt gcc acg aag caa cct ttt gag atc acc acc att gat 163  
 Ala Ile Val Arg Ala Thr Lys Gln Pro Phe Glu Ile Thr Thr Ile Asp  
                                   10                  15                  20  
 ctg gat gca cca cga cca gat gaa gtt caa atc cgt gtt att gct gcc 211  
 Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile Arg Val Ile Ala Ala  
                           25                  30                  35  
 gga gtg cgc cac act gac gca att gtt cgt gat cag att tac cca act 259  
 Gly Val Arg His Thr Asp Ala Ile Val Arg Asp Gln Ile Tyr Pro Thr  
           40                  45                  50  
 ttt ctt ccc gca gtt ttc ggc cac gaa ggc gcc gga gta gtt gtc gcc 307  
 Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala Gly Val Val Val Ala  
           55                  60                  65  
 gtg ggt tct gca gtc acc tcg gtg aaa cca gat gac aag gta gtg ctg 355  
 Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp Asp Lys Val Val Leu  
           70                  75                  80                  85  
 gga ttc aac tct tgt ggc cag tgc ttg aag tgt ttg ggc ggt aag cct 403  
 Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys Leu Gly Gly Lys Pro

90	95	100	
gcg tac tgt gag aaa ttc tat gac	cgc aac ttc gca tgc acc cgc gat	451	
Ala Tyr Cys Glu Lys Phe Tyr Asp	Arg Asn Phe Ala Cys Thr Arg Asp		
105	110	115	
gcc ggg cac act act ttg ttt acc cgt	gca aca aaa gag cag gca gag	499	
Ala Gly His Thr Thr Leu Phe Thr	Arg Ala Thr Lys Glu Gln Ala Glu		
120	125	130	
gcc atc atc gac acc ctt gat gat gtt	ttc tac gat gcg gat gcg ggt	547	
Ala Ile Ile Asp Thr Leu Asp Asp Val	Phe Tyr Asp Ala Asp Ala Gly		
135	140	145	
ttc ctg gca tac cca gca act ccc cca	gag gct tcg gga gta agc gtg	595	
Phe Leu Ala Tyr Pro Ala Thr Pro Pro	Glu Ala Ser Gly Val Ser Val		
150	155	160	
ttg gtt gtc gcg gct ggt acc tct gat	ctc ccc caa gca aag gaa gca	643	
Leu Val Val Ala Ala Gly Thr Ser Asp	Leu Pro Gln Ala Lys Glu Ala		
170	175	180	
cta cac act gcc tcc tac ttg ggg cgc	tcc acc tca ctg att gtt gat	691	
Leu His Thr Ala Ser Tyr Leu Gly Arg	Ser Thr Ser Leu Ile Val Asp		
185	190	195	
ttt gga gtg gct ggc atc cac cgc ctg	ctt tca tac gaa gaa gaa ctc	739	
Phe Gly Val Ala Gly Ile His Arg Leu	Leu Ser Tyr Glu Glu Glu Leu		
200	205	210	
cgc gct gcg ggc gtg ctc atc gtt gcc	gct gga atg gat ggt gcg cta	787	
Arg Ala Ala Gly Val Leu Ile Val Ala	Ala Gly Met Asp Gly Ala Leu		
215	220	225	
ccc gga gtt gtc gca ggc tta gtg tcc	gca cct gtc gtc gca ctg cca	835	
Pro Gly Val Val Ala Gly Leu Val Ser	Ala Pro Val Val Ala Leu Pro		
230	235	240	
acc tcc gtg gga tac ggc gca ggt gct	gga gga atc gca cca ctt ctg	883	
Thr Ser Val Gly Tyr Gly Ala Gly Ala	Gly Gly Ile Ala Pro Leu Leu		
250	255	260	
acc atg ctt aac gcc tgc gcg ccg gga	gtt gga gtg gtc aac att gat	931	
Thr Met Leu Asn Ala Cys Ala Pro Gly	Val Gly Val Val Asn Ile Asp		
265	270	275	
aac ggc tat gga gca gga cac ctg gct	gcg cag att gcg gcg agg	976	
Asn Gly Tyr Gly Ala Gly His Leu Ala	Ala Gln Ile Ala Ala Arg		
280	285	290	
taagggtttc gcaggagacg aac		999	

&lt;210&gt; 940

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 940

Met Gln Thr Leu Ala Ala Ile Val Arg Ala Thr Lys Gln Pro Phe Glu  
 1 5 10 15

Ile Thr Thr Ile Asp Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile  
                   20                                  25                                  30  
 Arg Val Ile Ala Ala Gly Val Arg His Thr Asp Ala Ile Val Arg Asp  
                   35                                  40                                  45  
 Gln Ile Tyr Pro Thr Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala  
                   50                                  55                                  60  
 Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp  
                   65                                  70                                  75                                  80  
 Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys  
                                   85                                  90                                  95  
 Leu Gly Gly Lys Pro Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe  
                   100                                  105                                  110  
 Ala Cys Thr Arg Asp Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr  
                   115                                  120                                  125  
 Lys Glu Gln Ala Glu Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr  
                   130                                  135                                  140  
 Asp Ala Asp Ala Gly Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala  
                   145                                  150                                  155                                  160  
 Ser Gly Val Ser Val Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro  
                                   165                                  170                                  175  
 Gln Ala Lys Glu Ala Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr  
                   180                                  185                                  190  
 Ser Leu Ile Val Asp Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser  
                   195                                  200                                  205  
 Tyr Glu Glu Glu Leu Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly  
                   210                                  215                                  220  
 Met Asp Gly Ala Leu Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro  
                   225                                  230                                  235                                  240  
 Val Val Ala Leu Pro Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly  
                                   245                                  250                                  255  
 Ile Ala Pro Leu Leu Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly  
                   260                                  265                                  270  
 Val Val Asn Ile Asp Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln  
                   275                                  280                                  285  
 Ile Ala Ala Arg  
                   290

&lt;210&gt; 941

&lt;211&gt; 1551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; RXA00619

&lt;400&gt; 941

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Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
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Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
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Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
                               70 75 80 85
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Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
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Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
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cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
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Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
                               135 140 145
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Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
                               150 155 160 165
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Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
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ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
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Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp Phe Asp Ala Val Ser	
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Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser Leu Ser His Thr Ile	
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Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu Gly Phe Lys Glu Gly	
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Gln Val Gly Ser Ser Ala Met Pro His Lys Met Asn Ala Arg Ser Cys	
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1363	
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 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val  
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 <213> Corynebacterium glutamicum  
  
 <400> 942  
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 Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly  
 35 40 45  
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp  
 50 55 60  
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His  
 65 70 75 80  
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu  
 85 90 95  
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu  
 100 105 110  
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile  
 115 120 125  
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu  
 130 135 140  
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu  
 145 150 155 160  
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu  
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly  
 180 185 190  
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu  
 195 200 205  
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe  
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 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp  
 225 230 235 240  
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser  
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 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu  
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 325 330 335  
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp  
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 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr  
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 370 375 380  
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 420 425 430  
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser  
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&lt;210&gt; 943

&lt;211&gt; 1683

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1660)

&lt;223&gt; RXA02622

&lt;400&gt; 943

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                                         Met Ser Asp Asp Arg
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aag gca att aaa cgc gca cta att agc gtg tat gac aag act ggc ctg 163
Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr Asp Lys Thr Gly Leu
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gag gat cta gcc cag gca ctt cac cgc gag aac gtg gaa att gtt tcc 211
Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn Val Glu Ile Val Ser
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acc gga tcc act gcg gcg aag att gct gag ctt ggt att cct gtt acc 259
Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu Gly Ile Pro Val Thr
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ccg gtt gag gag ctc acc ggt ttc cct gag tgc ctt gag ggc cgt gtg 307
Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys Leu Glu Gly Arg Val
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Lys Thr Leu His Pro Lys Val His Ala Gly Ile Leu Ala Asp Thr Arg
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Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile Asp Ile Gly Gly Pro
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              150              155              160              165

gga ttc tcc cgc gcg gag cgc acc aag ttg gct gct gag gct ttc cgc 643
Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala Ala Glu Ala Phe Arg
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cac acc gca acc tac gat gtc acc gtt gca acc tgg atg agc gag cag 691
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185										190										195										
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acc aac acc ttg tcc cgc agc ttg cgt tac ggt gag aac cct cac cag	787																													
Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly Glu Asn Pro His Gln																														
215 220 225																														
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gtt ctg aag gac ctg gag ttc gcg tgg act gca gtt cgt tcc gtg aag  
1363

Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys  
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1411

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425 430 435

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1459

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Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr  
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1603

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1651

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<210> 944

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 944

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35 40 45

Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys  
50 55 60

Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile  
65 70 75 80

Leu Ala Asp Thr Arg Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu  
                                     85                                    90                                    95  
 Glu Val Ala Pro Phe Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala  
                                     100                                    105                                    110  
 Glu Thr Val Ala Ser Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile  
                                     115                                    120                                    125  
 Asp Ile Gly Gly Pro Ser Met Val Arg Ala Ala Ala Lys Asn His Pro  
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 Ser Val Ala Val Val Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu  
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 Ala Leu Lys Thr Gly Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala  
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 Ala Glu Ala Phe Arg His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr  
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 Trp Met Ser Glu Gln Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro  
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 Gly Trp Ile Gly Thr Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly  
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 Glu Asn Pro His Gln Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly  
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 Leu Ala Gln Ala Lys Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn  
                                     245                                    250                                    255  
 Tyr Thr Asp Ser Asp Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg  
                                     260                                    265                                    270  
 Pro Cys Val Ala Ile Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val  
                                     275                                    280                                    285  
 Ser Asp Glu Ser Ile Ala Ala Ala His Arg Glu Ala His Ala Cys Asp  
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 Ser Val Ser Ala Phe Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser  
                                     305                                    310                                    315                                    320  
 Val Glu Met Ala Asn Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile  
                                     325                                    330                                    335  
 Ala Pro Ser Tyr Glu Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys  
                                     340                                    345                                    350  
 Asn Ile Arg Ile Leu Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu  
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 Ser Arg Glu Ile Ser Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile  
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 His Ala Glu Gly Asp Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser  
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Ala Val Ser Pro Glu Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala  
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Val Arg Ser Val Lys Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala  
 420 425 430

Thr Val Gly Val Gly Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg  
 435 440 445

Leu Ala Val Asp Arg Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala  
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Glu Ala Gly Ile Thr Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp  
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Asn Glu Val Ile Glu Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu  
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Thr Gly Ala Arg His Phe Ala His  
 515 520

&lt;210&gt; 945

&lt;211&gt; 1641

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1618)

&lt;223&gt; RXN00488

&lt;400&gt; 945

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 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly  
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 Leu Thr Phe Asp Asp Val Leu Leu Pro Asp Ala Ser Asp Val Val  
 25 30 35

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aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307  
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atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355  
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 70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt	403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg	
90 95 100	
tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg	451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met	
105 110 115	
agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt	499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly	
120 125 130	
ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac	547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn	
135 140 145	
cgc gat atg cgt ttt gaa agc gac atg aac cgt cgt gtc gct gaa gtt	595
Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val	
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Met Thr Pro Met Pro Leu Val Val Ala Glu Glu Gly Val Thr Lys Glu	
170 175 180	
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Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
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Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile Thr Val Lys Asp Phe	
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Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys Asp Ala Ser Gly Arg	
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Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu Glu Ser Phe Gln Arg	
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gct ggt gcg ctt gcc gac gcc ggc gtc gac att ttg gtc gta gac tct	883
Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile Leu Val Val Asp Ser	
250 255 260	
gca cac gcc cat agc cgt gga gtt ttg gac atg gtg tcc cgc gtg aag	931
Ala His Ala His Ser Arg Gly Val Leu Asp Met Val Ser Arg Val Lys	
265 270 275	
aag tcg ttc ccc aag gtc gat atc gtt ggc ggc aac ttg gcg acc cgc	979
Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly Asn Leu Ala Thr Arg	
280 285 290	
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1027	
Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala Asp Ala Ile Lys Val	
295 300 305	
ggt att ggc cca ggt tct att tgc acc act cgc gtt gtc gca ggt gtc	
1075	
Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val	

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1123
Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His
          330          335          340

aag gct ggc gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt
1171
Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly
          345          350          355

gat atc gct aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc
1219
Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly
          360          365          370

tcc atg ctg gct ggt acc gct gag gct cct ggt gag acc atc acc atc
1267
Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile
          375          380          385

aac ggc aag cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct
1315
Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala
390          395          400          405

atg cag ggc cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac
1363
Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp
          410          415          420

cgt tac ttc cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa
1411
Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu
          425          430          435

ggc atc gaa ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att
1459
Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile
          440          445          450

cac cag cag gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc
1507
His Gln Gln Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser
          455          460          465

tcc acc att gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc
1555
Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser
470          475          480          485

gcg ggt ctg aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa
1603
Ala Gly Leu Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu
          490          495          500

gct cct aac tac cac tagattttgc tcacttaaag agc
1641
Ala Pro Asn Tyr His
          505

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<210> 946  
 <211> 506  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 946

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Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
 1              5              10              15

Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
      20              25              30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
      35              40              45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
      50              55              60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
      65              70              75              80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
      85              90              95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
      100             105             110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
      115             120             125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
      130             135             140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg
      145             150             155             160

Arg Val Ala Glu Val Met Thr Pro Met Pro Leu Val Val Ala Glu Glu
      165             170             175

Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val
      180             185             190

Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile
      195             200             205

Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys
      210             215             220

Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu
      225             230             235             240

Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile
      245             250             255

Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met
      260             265             270

Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly
      275             280             285

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Asn Leu Ala Thr Arg Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala  
290 295 300

Asp Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg  
305 310 315 320

Val Val Ala Gly Val Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala  
325 330 335

Ala Val Pro Ala His Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly  
340 345 350

Met Gln Phe Ser Gly Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn  
355 360 365

Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly  
370 375 380

Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met  
385 390 395 400

Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg  
405 410 415

Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp  
420 425 430

Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro  
435 440 445

Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met  
450 455 460

Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe  
465 470 475 480

Val Gln Ile Thr Ser Ala Gly Leu Lys Glu Ser His Pro His His Ile  
485 490 495

Gln Gln Thr Val Glu Ala Pro Asn Tyr His  
500 505

<210> 947

<211> 574

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> FRXA00492

<400> 947

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tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115  
Met Thr Thr Gln Ser  
1 5



cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163  
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly  
                   10                  15                  20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211  
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val  
                   25                  30                  35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259  
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu  
                   40                  45                  50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307  
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg  
                   55                  60                  65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355  
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg  
                   70                  75                  80                  85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403  
 Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg  
                   90                  95                  100

tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451  
 Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met  
                   105                  110                  115

agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499  
 Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly  
                   120                  125                  130

ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547  
 Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn  
                   135                  140                  145

cgc gat atg cgt ttt gaa agc gac atg 574  
 Arg Asp Met Arg Phe Glu Ser Asp Met  
                   150                  155

&lt;210&gt; 948

&lt;211&gt; 158

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 948

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys  
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Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp  
                   20                  25                  30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr  
                   35                  40                  45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr  
                   50                  55                  60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile  
                   65                  70                  75                  80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val  
                             85                            90                            95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr  
                             100                            105                            110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg  
                             115                            120                            125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val  
                             130                            135                            140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met  
 145                            150                            155

&lt;210&gt; 949

&lt;211&gt; 557

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(534)

&lt;223&gt; FRXA00488

&lt;400&gt; 949

cag atc act gcg atc atg gag gca gct gtt cca gct cac aag gct ggc	48
Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly	
1                            5                            10                            15	
ggt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt gat atc gct	96
Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala	
20                            25                            30	
aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc tcc atg ctg	144
Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu	
35                            40                            45	
gct ggt acc gct gag gct cct ggt gag acc atc acc atc aac ggc aag	192
Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys	
50                            55                            60	
cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct atg cag ggc	240
Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly	
65                            70                            75                            80	
cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac cgt tac ttc	288
Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe	
85                            90                            95	
cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa ggc atc gaa	336
Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu	
100                            105                            110	
ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att cac cag cag	384
Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln	
115                            120                            125	
gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc tcc acc att	432

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile  
 130 135 140

gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc gcg ggt ctg 480  
 Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu  
 145 150 155 160

aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa gct cct aac 528  
 Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn  
 165 170 175

tac cac tagattttgc tcacttaaagc agc 557  
 Tyr His

<210> 950  
 <211> 178  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 950  
 Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly  
 1 5 10 15

Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala  
 20 25 30

Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu  
 35 40 45

Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys  
 50 55 60

Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly  
 65 70 75 80

Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe  
 85 90 95

Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu  
 100 105 110

Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln  
 115 120 125

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile  
 130 135 140

Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu  
 145 150 155 160

Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn  
 165 170 175

Tyr His

<210> 951  
 <211> 1554

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1531)

&lt;223&gt; RXA02469

&lt;400&gt; 951

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cgctcgaaaag cagtagtaaa gcagcaggaa ggtgggtggaa agagcaattg aggtaccctt 60
gccgtgttca gggataactg attaatcaac taggagaccc atg cgt ttt ctt aac 115
                                         Met Arg Phe Leu Asn
                                         1           5

aat tcc aat ccg ccc tat gag ctg aca tat tcc gat gtg ttt atg gtg 163
Asn Ser Asn Pro Tyr Glu Leu Thr Tyr Ser Asp Val Phe Met Val
          10          15          20

cct tcg cgt tct gac gta ggc tcc cgc atg tcc gtg gat ctg cgc acc 211
Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser Val Asp Leu Arg Thr
          25          30          35

aat gac gga act gga aca acc atc ccg ctc gtt gtg gca aac atg act 259
Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val Val Ala Asn Met Thr
          40          45          50

gct gtt gct ggc cga cgc atg gct gag acc att gcg cgc cgc ggt ggc 307
Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile Ala Arg Arg Gly Gly
          55          60          65

atg gcg att ctt ccg cag gat gtg ccc gcc gat att gct gca gag act 355
Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp Ile Ala Ala Glu Thr
          70          75          80          85

atc gcg aat gtg aag aaa gcg gac ctg gtt ttt gat acc cca att acc 403
Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr
          90          95          100

gta aaa ccg cac cac acc gtg ggt tat gca cgc aac ttg atc cac aag 451
Val Lys Pro His His Thr Val Gly Tyr Ala Arg Asn Leu Ile His Lys
          105          110          115

cgt gcg cac ggt gca gcc att gtt ttg gag ggc gat cag ccg gtc ggc 499
Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly Asp Gln Pro Val Gly
          120          125          130

atc gtc acc gac aag gac ctc gaa ggc gca gac aac ttc act cag gtg 547
Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val
          135          140          145

ggc acc ctc atg tcc acc tcc cta ttg acg ctg cct gag gat att tcc 595
Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu Pro Glu Asp Ile Ser
          150          155          160          165

ccc gaa gac gcc ttc gga atc ctc cac gaa cac agc cgc aaa ctc gcc 643
Pro Glu Asp Ala Phe Gly Ile Leu His Glu His Ser Arg Lys Leu Ala
          170          175          180

ccc gtc gtc gcg gct gac ggc tca ctc cgc ggc atc ctc acc cgc acc 691
Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly Ile Leu Thr Arg Thr

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185	190	195	
ggc gcc ctg cgc gcc acc atg tac aag ccg gct atc gac gcc aac ggc Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala Ile Asp Ala Asn Gly 200 205 210			739
cgc ctg cga gtc ggc gcc gcc atc ggc atc aac ggc gac atc gaa gga Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn Gly Asp Ile Glu Gly 215 220 225			787
cgc acc aaa acg ctt ctc gac gcc ggc gcc gac gtt cta gtc gtc gac Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp Val Leu Val Val Asp 230 235 240 245			835
aca gca cac ggc cac caa tcc acc atg atc agc gcc ctc aaa cgc atc Thr Ala His Gly His Gln Ser Thr Met Ile Ser Ala Leu Lys Arg Ile 250 255 260			883
cgc gca ctc gac gtc aac gtc ccc atc gtt gct ggc aac gtg gtc acc Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala Gly Asn Val Val Thr 265 270 275			931
gcc gat ggt gtc cgc gac cta gtt gaa gca ggc gca aac atc atc aag Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asn Ile Ile Lys 280 285 290			979
gta ggc gtt gga cca ggc gca atg tgc acc acc cgc atg caa acc ggc 1027 Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Gln Thr Gly 295 300 305			
gtt ggc cga cca cag ttc tcc gca gtg ctg gaa tgc gca gcc gaa gcc 1075 Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu Cys Ala Ala Glu Ala 310 315 320 325			
cgc aaa ctc ggc gca cac gta tgg gca gac ggc gga gtc cgc gac ccc 1123 Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly Gly Val Arg Asp Pro 330 335 340			
cgc gac gtc gcc ctg gca ctc gca gct ggc gcc tcc aac gtg atg gtc 1171 Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala Ser Asn Val Met Val 345 350 355			
gga tcc tgg ttc tcc gga acc tac gaa tcc ccc ggc gac ctc cgc ttc 1219 Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro Gly Asp Leu Arg Phe 360 365 370			
gaa tcc gac gga cgc atg tac aaa gaa tcc ttc ggt atg gca tcc cgg 1267 Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe Gly Met Ala Ser Arg 375 380 385			
cgc gcc gtg gaa agc cga aac caa aag gtc gaa gct ttc gaa aaa gca 1315 Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu Ala Phe Glu Lys Ala 390 395 400 405			

cgc cgc gca atg ttc gaa gaa ggc atc tcc act gcc cgc atc tac att  
1363

Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr Ala Arg Ile Tyr Ile  
410 415 420

gac aaa cgc cac ggc gga gtc gag gac ctg gta gat caa atc atc tcc  
1411

Asp Lys Arg His Gly Gly Val Glu Asp Leu Val Asp Gln Ile Ile Ser  
425 430 435

ggc gtc cgc tcc tca ttc acc tac gca ggc gcc gat tcg att gaa acc  
1459

Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala Asp Ser Ile Glu Thr  
440 445 450

ttc ttc gaa cgc gcc acc gtc gga gtt caa tcc acc gaa ggc tac gca  
1507

Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser Thr Glu Gly Tyr Ala  
455 460 465

gaa gga aag cca cgc gct tcg cgt taagtgttgt tgtgcctttg aga  
1554

Glu Gly Lys Pro Arg Ala Ser Arg  
470 475

<210> 952

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 952

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20 25 30

Val Asp Leu Arg Thr Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val  
35 40 45

Val Ala Asn Met Thr Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile  
50 55 60

Ala Arg Arg Gly Gly Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp  
65 70 75 80

Ile Ala Ala Glu Thr Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe  
85 90 95

Asp Thr Pro Ile Thr Val Lys Pro His His Thr Val Gly Tyr Ala Arg  
100 105 110

Asn Leu Ile His Lys Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly  
115 120 125

Asp Gln Pro Val Gly Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp  
130 135 140

Asn Phe Thr Gln Val Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu  
145 150 155 160

Pro Glu Asp Ile Ser Pro Glu Asp Ala Phe Gly Ile Leu His Glu His  
 165 170 175  
 Ser Arg Lys Leu Ala Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly  
 180 185 190  
 Ile Leu Thr Arg Thr Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala  
 195 200 205  
 Ile Asp Ala Asn Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn  
 210 215 220  
 Gly Asp Ile Glu Gly Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp  
 225 230 235 240  
 Val Leu Val Val Asp Thr Ala His Gly His Gln Ser Thr Met Ile Ser  
 245 250 255  
 Ala Leu Lys Arg Ile Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala  
 260 265 270  
 Gly Asn Val Val Thr Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly  
 275 280 285  
 Ala Asn Ile Ile Lys Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr  
 290 295 300  
 Arg Met Gln Thr Gly Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu  
 305 310 315 320  
 Cys Ala Ala Glu Ala Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly  
 325 330 335  
 Gly Val Arg Asp Pro Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala  
 340 345 350  
 Ser Asn Val Met Val Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro  
 355 360 365  
 Gly Asp Leu Arg Phe Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe  
 370 375 380  
 Gly Met Ala Ser Arg Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu  
 385 390 395 400  
 Ala Phe Glu Lys Ala Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr  
 405 410 415  
 Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val  
 420 425 430  
 Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala  
 435 440 445  
 Asp Ser Ile Glu Thr Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser  
 450 455 460  
 Thr Glu Gly Tyr Ala Glu Gly Lys Pro Arg Ala Ser Arg  
 465 470 475

<210> 953  
 <211> 1692  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1669)  
 <223> RXN00487

<400> 953

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                                   Val Ser Leu Gln Thr
                                   1 5
aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163
Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln
              10              15              20
ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211
Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile
              25              30              35
ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259
Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala
              40              45              50
ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307
Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro
              55              60              65
tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att 355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile
              70              75              80              85
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc 403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala
              90              95              100
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt 451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly
              105              110              115
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc 499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser
              120              125              130
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg 547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala
              135              140              145
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa 595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys
              150              155              160              165
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc 643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly
              170              175              180

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cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	
1027	
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	
tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt	
1075	
Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly	
310 315 320 325	
tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg	
1123	
Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val	
330 335 340	
gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac	
1171	
Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn	
345 350 355	
gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg	
1219	
Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu	
360 365 370	
cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc	
1267	
Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly	
375 380 385	
ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt	
1315	

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu  
 390 395 400 405  
 ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc  
 1363  
 Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu  
 410 415 420  
 cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt  
 1411  
 Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu  
 425 430 435  
 gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc  
 1459  
 Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg  
 440 445 450  
 tct gtt ggt gtt caa ggc gat ggc cgc acc tac gga cac cca atc gtg  
 1507  
 Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr Gly His Pro Ile Val  
 455 460 465  
 ctg cgc cca gtg tct tcc gaa gac gca atg acc gcc gac tgg acc cgc  
 1555  
 Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr Ala Asp Trp Thr Arg  
 470 475 480 485  
 ctg cca tac gag gtt ctg gag aag atc tcc acc cgc atc acc aac gaa  
 1603  
 Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr Arg Ile Thr Asn Glu  
 490 495 500  
 gtt cca gat gtg aac cgc gtg gtg ctg gac gta acc tcc aag cca cca  
 1651  
 Val Pro Asp Val Asn Arg Val Val Leu Asp Val Thr Ser Lys Pro Pro  
 505 510 515  
 gga acc atc gaa tgg gag taggccttaa atgagccttc gtt  
 1692  
 Gly Thr Ile Glu Trp Glu  
 520

&lt;210&gt; 954

&lt;211&gt; 523

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 954

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly  
 1 5 10 15  
 Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile  
 20 25 30  
 Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala  
 35 40 45  
 Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr  
 50 55 60

Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu  
 65 70 75 80  
 Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu  
 85 90 95  
 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp  
 100 105 110  
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His  
 115 120 125  
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly  
 130 135 140  
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu  
 145 150 155 160  
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu  
 165 170 175  
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile  
 180 185 190  
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu  
 195 200 205  
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys  
 210 215 220  
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln  
 225 230 235 240  
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu  
 245 250 255  
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala  
 260 265 270  
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser  
 275 280 285  
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly  
 290 295 300  
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu  
 305 310 315 320  
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu  
 325 330 335  
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile  
 340 345 350  
 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys  
 355 360 365  
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val  
 370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe  
 385 390 395 400  
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp  
 405 410 415  
 Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu  
 420 425 430  
 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu  
 435 440 445  
 Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr  
 450 455 460  
 Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr  
 465 470 475 480  
 Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr  
 485 490 495  
 Arg Ile Thr Asn Glu Val Pro Asp Val Asn Arg Val Val Leu Asp Val  
 500 505 510  
 Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu  
 515 520

<210> 955  
 <211> 1486  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1486)  
 <223> FRXA00487

<400> 955  
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 agaatcttat ttggaggctc gtctagtaga gtgagttctt gtg agc ctt cag aca 115  
 Val Ser Leu Gln Thr  
 1 5  
 aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163  
 Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln  
 10 15 20  
 ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211  
 Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile  
 25 30 35  
 ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259  
 Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala  
 40 45 50  
 ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307  
 Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro  
 55 60 65

tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att	355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile	
70 75 80 85	
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc	403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala	
90 95 100	
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt	451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly	
105 110 115	
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser	
120 125 130	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
135 140 145	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
150 155 160 165	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
170 175 180	
cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	
1027	
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt  
1075

Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly  
310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg  
1123

Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val  
330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac  
1171

Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn  
345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg  
1219

Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu  
360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc  
1267

Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly  
375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt  
1315

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu  
390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc  
1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu  
410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt  
1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu  
425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc  
1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg  
440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc  
1486

Ser Val Gly Val Gln Gly Asp Gly Arg  
455 460

<210> 956

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 956

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly  
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Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile

20	25	30
Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala 35 40 45		
Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr 50 55 60		
Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu 65 70 75 80		
Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu 85 90 95		
Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp 100 105 110		
Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His 115 120 125		
Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly 130 135 140		
Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu 145 150 155 160		
Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu 165 170 175		
His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile 180 185 190		
Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu 195 200 205		
Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys 210 215 220		
Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln 225 230 235 240		
Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu 245 250 255		
Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala 260 265 270		
Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser 275 280 285		
Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly 290 295 300		
Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu 305 310 315 320		
Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu 325 330 335		
Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile 340 345 350		

Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys  
 355 360 365  
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val  
 370 375 380  
 Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe  
 385 390 395 400  
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp  
 405 410 415  
 Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu  
 420 425 430  
 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu  
 435 440 445  
 Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg  
 450 455 460

&lt;210&gt; 957

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(670)

&lt;223&gt; RXA02237

&lt;400&gt; 957

gacgagctgg gcattgctca gacccgctcgt cttcgtggac tgggtgaccg tcagcgtcgc 60  
 gcacttctcg agcggttctgg cttcagaggat taattcttca gtg tgc ggc gat aac 115  
 Val Ser Gly Asp Asn  
 1 5  
 caa cta gga cgg ctc gta att ctt gcg ggc ccc tca gcg gtc ggt aaa 163  
 Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro Ser Ala Val Gly Lys  
 10 15 20  
 tcg act gtg gtt gat cgc ctc cgc aat gac gtt cca aac ctg tat ttc 211  
 Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val Pro Asn Leu Tyr Phe  
 25 30 35  
 agt gtg tgc atg acc act agg gca cct cgt cct ggt gaa gtc gat gga 259  
 Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro Gly Glu Val Asp Gly  
 40 45 50  
 cgt gac tac ttc tat gtc act gca cag gaa ttt cag gac aaa atc gac 307  
 Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe Gln Asp Lys Ile Asp  
 55 60 65  
 tgt gga gag atg ctt gaa tgg gca gat atc cac ggc ggt ttg cag cgt 355  
 Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His Gly Gly Leu Gln Arg  
 70 75 80 85  
 tca ggc act cca gca ggt ccc gtc aat gag gct cgc caa aat ggt cgg 403



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<210> 958
<211> 190
<212> PRT
<213> Corynebacterium glutamicum
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Val	Ser	Gly	Asp	Asn	Gln	Leu	Gly	Arg	Leu	Val	Ile	Leu	Ala	Gly	Pro
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Ser	Ala	Val	Gly	Lys	Ser	Thr	Val	Val	Asp	Arg	Leu	Arg	Asn	Asp	Val
			20					25					30		
Pro	Asn	Leu	Tyr	Phe	Ser	Val	Ser	Met	Thr	Thr	Arg	Ala	Pro	Arg	Pro
		35					40					45			
Gly	Glu	Val	Asp	Gly	Arg	Asp	Tyr	Phe	Tyr	Val	Thr	Ala	Gln	Glu	Phe
	50					55					60				
Gln	Asp	Lys	Ile	Asp	Cys	Gly	Glu	Met	Leu	Glu	Trp	Ala	Asp	Ile	His
65					70					75					80
Gly	Gly	Leu	Gln	Arg	Ser	Gly	Thr	Pro	Ala	Gly	Pro	Val	Asn	Glu	Ala
				85					90					95	
Arg	Gln	Asn	Gly	Arg	Pro	Val	Leu	Val	Glu	Val	Asp	Leu	Ala	Gly	Ala
			100					105					110		
Arg	Asn	Ile	Ala	Ser	Leu	Ile	Pro	Asp	Ala	Glu	Thr	Ile	Phe	Leu	Ala
	115						120					125			
Pro	Pro	Ser	Trp	Glu	Val	Leu	Val	Glu	Arg	Leu	Thr	Gly	Arg	Gly	Thr

130	135	140	
Glu Ser Glu Asp Val	Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu		
145	150	155	160
Leu Ala Ala Gln Ser Glu Phe Lys His Val	Ile Ile Asn Asp Asp Val		
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Asp Thr Ala Val Lys Ala Ile Glu Asp Val	Leu Leu Gly Ala		
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<210> 959			
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<212> DNA			
<213> Corynebacterium glutamicum			
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<221> CDS			
<222> (101) .. (1390)			
<223> RXA01446			
<400> 959			
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tgcatactcc aacttcattg atcggatgtg acgtaaacca atg gct gca atc gtt 115			
		Met Ala Ala Ile Val	
		1 5	
att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat 163			
Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp			
	10	15	20
att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac 211			
Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn			
	25	30	35
aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag 259			
Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys			
	40	45	50
ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc 307			
Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly			
	55	60	65
aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc 355			
Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly			
	70	75	80
ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac 403			
Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn			
	90	95	100
gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa 451			
Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu			
	105	110	115
cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc 499			
Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly			
	120	125	130

cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac 547  
 Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp  
 135 140 145

att ttc gac gaa tcc atc ctt cgt caa aaa gtc gaa tcc gcc ctg gat 595  
 Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp  
 150 155 160 165

tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc 643  
 Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val  
 170 175 180

gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc 691  
 Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg  
 185 190 195

ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag 739  
 Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln  
 200 205 210

ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg 787  
 Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val  
 215 220 225

gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt 835  
 Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly  
 230 235 240 245

ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc 883  
 Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser  
 250 255 260

ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc 931  
 Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe  
 265 270 275

cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt 979  
 Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly  
 280 285 290

ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac  
 1027  
 Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr  
 295 300 305

gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac  
 1075  
 Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp  
 310 315 320 325

tac ttc ctg acc aag cta gac gtg ctc acc ggc atc ggt gaa atc cca  
 1123  
 Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro  
 330 335 340

atc tgc gta gct tac gac gtt gat ggt gtt cgc cac gat gaa atg cca  
 1171  
 Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro  
 345 350 355

ctg acc cag tca gag ttc cac cac gca acc cca atc ttt gaa acc atg  
1219

Leu Thr Gln Ser Glu Phe His His Ala Thr Pro Ile Phe Glu Thr Met  
360 365 370

cct gca tgg gac gaa gac atc acc gac tgc aag acc ttc gag gat ctt  
1267

Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys Thr Phe Glu Asp Leu  
375 380 385

cca caa aag gcc cag gac tac gtc cga cgt ctg gaa gaa ctc tct ggt  
1315

Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu Glu Glu Leu Ser Gly  
390 395 400 405

gct cgc ttc tcc tac atc ggt gtt gga cct ggt cgc gat cag acc atc  
1363

Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly Arg Asp Gln Thr Ile  
410 415 420

gtc ctg cat gac gta cta gct gac aac tagtactgat aaacatcagt  
1410

Val Leu His Asp Val Leu Ala Asp Asn  
425 430

gag  
1413

<210> 960

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 960

Met Ala Ala Ile Val Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys  
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Gly Lys Ala Thr Asp Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys  
20 25 30

Pro Asn Gly Gly Asn Asn Ala Gly His Thr Val Val Val Gly Gly Glu  
35 40 45

Lys Tyr Glu Leu Lys Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala  
50 55 60

Thr Pro Ile Leu Gly Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe  
65 70 75 80

Glu Glu Ile Asp Gly Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu  
85 90 95

Arg Ile Ser Ala Asn Ala His Leu Val Ala Pro Tyr His Gln Val Met  
100 105 110

Asp Arg Val Gln Glu Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr  
115 120 125

Gly Arg Gly Ile Gly Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly  
130 135 140

Ile Arg Val Gln Asp Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val  
 145 150 155 160  
 Glu Ser Ala Leu Asp Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn  
 165 170 175  
 Arg Lys Ala Ile Val Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr  
 180 185 190  
 Ala Asp Arg Leu Arg Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn  
 195 200 205  
 Glu Ala Leu Asp Gln Gly Lys His Val Leu Met Glu Gly Gly Gln Ala  
 210 215 220  
 Thr Met Leu Asp Val Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser  
 225 230 235 240  
 Asn Pro Thr Ala Gly Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr  
 245 250 255  
 Lys Ile Thr Ser Ser Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val  
 260 265 270  
 Gly Ala Gly Pro Phe Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr  
 275 280 285  
 Leu Gln Thr Val Gly Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg  
 290 295 300  
 Arg Cys Gly Trp Tyr Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val  
 305 310 315 320  
 Asn Gly Phe Thr Asp Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly  
 325 330 335  
 Ile Gly Glu Ile Pro Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg  
 340 345 350  
 His Asp Glu Met Pro Leu Thr Gln Ser Glu Phe His His Ala Thr Pro  
 355 360 365  
 Ile Phe Glu Thr Met Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys  
 370 375 380  
 Thr Phe Glu Asp Leu Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu  
 385 390 395 400  
 Glu Glu Leu Ser Gly Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly  
 405 410 415  
 Arg Asp Gln Thr Ile Val Leu His Asp Val Leu Ala Asp Asn  
 420 425 430

&lt;210&gt; 961

&lt;211&gt; 1551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1528)  
 <223> RXA00619

<400> 961

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cgactagggtt agtttcgggtt cgtggggaat aataatttgc gtg gct gat aaa aag 115
                               Val Ala Asp Lys Lys
                               1 5

aag atc gca aac gtc ctg tgc aac cgt tac gcc tcc gcg gaa ctt tct 163
Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
                               10 15 20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
                               25 30 35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
                               40 45 50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
                               55 60 65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
                               70 75 80 85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403
Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
                               90 95 100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
                               105 110 115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
                               120 125 130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
                               135 140 145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
                               150 155 160 165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
                               170 175 180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
                               185 190 195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739
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Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu Ala Arg Leu Ser Asp	
200	205 210
ctg gaa acc cgc atc gca gca cac ctc ggc ttt gat cgc gtc ttc gac	787
Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe Asp Arg Val Phe Asp	
215	220 225
tcc gtc ggc cag gtc tac cca cgt tcc ctt gac ttc gat gca gta tct	835
Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp Phe Asp Ala Val Ser	
230	235 240 245
gct ctg gtt cag ctt ggc tcc ggc cca tca tcg ctg tcc cac acc att	883
Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser Leu Ser His Thr Ile	
	250 255 260
cgt ctc atg gcc ggc acc gaa act gtt acc gaa ggt ttt aag gaa ggc	931
Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu Gly Phe Lys Glu Gly	
	265 270 275
cag gtc ggt tcc tct gca atg cct cac aag atg aac gct cgc tcc tgt	979
Gln Val Gly Ser Ser Ala Met Pro His Lys Met Asn Ala Arg Ser Cys	
	280 285 290
gag cgc gtg ggc ggc ctg cag gtt att ctt cgc gga tac ctc acc atg	
1027	
Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg Gly Tyr Leu Thr Met	
	295 300 305
gtt gct gat ctt tcc ggc cag cag tgg aac gaa ggc gat gtc ttc tgc	
1075	
Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu Gly Asp Val Phe Cys	
310	315 320 325
tcc gtg atc cgc cgc gtt gca ctg cca gac gca ttc ttc gcg att gac	
1123	
Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala Phe Phe Ala Ile Asp	
	330 335 340
gga atg ttt gaa act ttc ctg aca gtc ctg gat gaa ttc ggt gca ttc	
1171	
Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp Glu Phe Gly Ala Phe	
	345 350 355
cct gcc atg atc gag cgc gaa ctt gag cgt tac ctg cca ttc ctg gca	
1219	
Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr Leu Pro Phe Leu Ala	
	360 365 370
act acc cgt atc ctc atg gcc gct gtc cgc gca ggc gtt ggc cgc gaa	
1267	
Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala Gly Val Gly Arg Glu	
	375 380 385
acc gca cac gaa gta atc aag gaa aac gct gtc gcg gtt gcc ctc aac	
1315	
Thr Ala His Glu Val Ile Lys Glu Asn Ala Val Ala Val Ala Leu Asn	
390	395 400 405
atg cgc gaa aat ggc ggt gac cag gac ctt atc cag cgc ctc gct gct	
1363	
Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile Gln Arg Leu Ala Ala	

410 415 420  
 gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct  
 1411  
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala  
 425 430 435  
 gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg  
 1459  
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val  
 440 445 450  
 ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac  
 1507  
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp  
 455 460 465  
 tac cga cca ggt gag att ctt taaaggtttt taacggcggtt cac  
 1551  
 Tyr Arg Pro Gly Glu Ile Leu  
 470 475  
  
 <210> 962  
 <211> 476  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 962  
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 Ser Ala Glu Leu Ser Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met  
 20 25 30  
 Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly  
 35 40 45  
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp  
 50 55 60  
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His  
 65 70 75 80  
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu  
 85 90 95  
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu  
 100 105 110  
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile  
 115 120 125  
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu  
 130 135 140  
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu  
 145 150 155 160  
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu  
 165 170 175



Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly  
 180 185 190  
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu  
 195 200 205  
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe  
 210 215 220  
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp  
 225 230 235 240  
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser  
 245 250 255  
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu  
 260 265 270  
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met  
 275 280 285  
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg  
 290 295 300  
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu  
 305 310 315 320  
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala  
 325 330 335  
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp  
 340 345 350  
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr  
 355 360 365  
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala  
 370 375 380  
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val  
 385 390 395 400  
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile  
 405 410 415  
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu  
 420 425 430  
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser  
 435 440 445  
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His  
 450 455 460  
 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu  
 465 470 475

&lt;210&gt; 963

&lt;211&gt; 666

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(643)

&lt;223&gt; RXA00688

&lt;400&gt; 963

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gcggaaccgc aatcttgatt cttgtatctg ttgcactgac cacagtgaag cagattgaga 60

gccagctcct gcaaagcaac tacgaaggac ttctaaaata atg cga ctc gta ctc 115
                                         Met Arg Leu Val Leu
                                         1 5

ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
                        10 15 20

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
                        25 30 35

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
                        40 45 50

gac gct ggc aag ctg gtt cca acc gac gtg act gca cgt atg gtt gct 307
Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
                        55 60 65

tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
                        70 75 80 85

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
                        90 95 100

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
                        105 110 115

gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
                        120 125 130

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
                        135 140 145

cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
                        150 155 160 165

ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu Lys Ala Leu Gly Lys
                        170 175 180

taagatttct tctctagtgc tgc 666

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<210> 964  
 <211> 181  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 964

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Met Arg Leu Val Leu Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln
  1             5             10             15

Ala Ala Ile Leu Ser Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly
          20             25             30

Asp Leu Phe Arg Ala Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu
      35             40             45

Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr
      50             55             60

Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly
      65             70             75             80

Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu
          85             90             95

Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn
      100             105             110

Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly
      115             120             125

Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr
      130             135             140

Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile
      145             150             155             160

Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu
          165             170             175

Lys Ala Leu Gly Lys
          180
  
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<210> 965  
 <211> 531  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA00266

<400> 965

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agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115
              Met Thr Glu Arg Thr
              1             5
  
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ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163  
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu  
                   10                  15                  20

atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211  
 Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp  
                   25                  30                  35

ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259  
 Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His  
                   40                  45                  50

gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307  
 Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala  
                   55                  60                  65

cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355  
 Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp  
                   70                  75                  80                  85

cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403  
 Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly  
                   90                  95                  100

acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451  
 Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His  
                   105                  110                  115

ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499  
 Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe  
                   120                  125                  130

cct aac ctg taattttttac ggtagaaaa aaa 531  
 Pro Asn Leu  
                   135

&lt;210&gt; 966

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 966

Met Thr Glu Arg Thr Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn  
                   1                  5                  10                  15

Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys  
                   20                  25                  30

Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys  
                   35                  40                  45

His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu  
                   50                  55                  60

Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg  
                   65                  70                  75                  80

Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala  
                   85                  90                  95

Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly  
 100 105 110

Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu  
 115 120 125

Ile Ser Ile Trp Phe Pro Asn Leu  
 130 135

<210> 967  
 <211> 1245  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1222)  
 <223> RXA00489

<400> 967  
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gtcttcgctg tatacgacca tttaagggag gcccgtcaca atg cgt gac cac gtt 115  
 Met Arg Asp His Val  
 1 5

gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163  
 Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr Tyr Ser Leu Asp Asp  
 10 15 20

att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211  
 Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp  
 25 30 35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat 259  
 Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn  
 40 45 50

cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc 307  
 His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly  
 55 60 65

aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc 355  
 Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg  
 70 75 80 85

cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag 403  
 His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu  
 90 95 100

gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca 451  
 Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala  
 105 110 115

gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt 499  
 Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg  
 120 125 130

gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt 547  
 Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg

135	140	145	
gag atc gca cca atc gtc atc aag gca ggt gct gat ctg ctg gtt atc Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala Asp Leu Leu Val Ile 150 155 160 165			595
cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala 170 175 180			643
ctg aac cta aag gaa ttc atc ggt tct ttg gat gtt cct gtc atc gct Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp Val Pro Val Ile Ala 185 190 195			691
ggt ggc gtg aac gat tac acc acc gcg ttg cac atg atg cgt acc ggt Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His Met Met Arg Thr Gly 200 205 210			739
gct gtg ggc atc atc gtc ggt ggc ggc gag aac acc aac agc cta gca Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn Thr Asn Ser Leu Ala 215 220 225			787
ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala 230 235 240 245			835
gca cgt cgt gat tac ctg gat gag acc ggt gga cgt tac gtg cac atc Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly Arg Tyr Val His Ile 250 255 260			883
att gca gat gga agc att gaa aac tcc ggt gat gta gtc aag gct att Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp Val Val Lys Ala Ile 265 270 275			931
gcc tgt ggc gca gat gct gtg gtg ctg ggt tca ccg ttg gct cgc gct Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser Pro Leu Ala Arg Ala 280 285 290			979
gaa gaa gct gct gga aag ggc tac ttc tgg cca gca gtg gca gcg cac 1027 Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro Ala Val Ala Ala His 295 300 305			
cct cgt ttc cca cgc ggt gtg gtt act gag tcc gtg gac ttg gat gag 1075 Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser Val Asp Leu Asp Glu 310 315 320 325			
gca gca cca agc ttg gag cag att ctg cat ggt ccg tct acg atg ccg 1123 Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly Pro Ser Thr Met Pro 330 335 340			
tgg ggt gtg gaa aac ttc gaa ggt gga tta aag cgt gcg ctg gct aag 1171 Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys Arg Ala Leu Ala Lys 345 350 355			
tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt 1219 Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys Val Ser Leu His Val			

360

365

370

aac taggtgtgtg tactgcctc ttc  
1245  
Asn

&lt;210&gt; 968

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 968

Met Arg Asp His Val Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr  
1 5 10 15  
Tyr Ser Leu Asp Asp Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser  
20 25 30  
Ser Lys Asp Val Asp Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp  
35 40 45  
Leu Pro Phe Met Asn His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe  
50 55 60  
Val Ile Glu Met Gly Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu  
65 70 75 80  
Gly Leu Trp Gly Arg His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val  
85 90 95  
Ile Ala Ala Tyr Glu Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu  
100 105 110  
Gln Glu Leu His Ala Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg  
115 120 125  
Ile Ala Gln Val Arg Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser  
130 135 140  
Pro Gln Asn Val Arg Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala  
145 150 155 160  
Asp Leu Leu Val Ile Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn  
165 170 175  
Thr Gly Gly Glu Ala Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp  
180 185 190  
Val Pro Val Ile Ala Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His  
195 200 205  
Met Met Arg Thr Gly Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn  
210 215 220  
Thr Asn Ser Leu Ala Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile  
225 230 235 240  
Ala Asp Val Ala Ala Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly  
245 250 255

Arg Tyr Val His Ile Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp  
 260 265 270  
 Val Val Lys Ala Ile Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser  
 275 280 285  
 Pro Leu Ala Arg Ala Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro  
 290 295 300  
 Ala Val Ala Ala His Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser  
 305 310 315 320  
 Val Asp Leu Asp Glu Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly  
 325 330 335  
 Pro Ser Thr Met Pro Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys  
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 Val Ser Leu His Val Asn  
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<210> 969  
 <211> 1545  
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<220>  
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 <222> (101)..(1531)  
 <223> RXN02281

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 Val Gln Lys Asp Ser  
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 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
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 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35  
 aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50  
 gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
 55 60 65  
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 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg



70	75	80	85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat				403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	90	95	100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg				451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt				499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac				547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	135	140	145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg				595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc				643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg				691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg				739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca				787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	215	220	225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa				835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc				883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca				931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa				979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	280	285	290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc				1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	295	300	305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att				1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile  
 310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
 1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac  
 1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp  
 345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac  
 1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn  
 360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc  
 1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser  
 375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga  
 1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly  
 390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg  
 1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu  
 410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac  
 1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr  
 425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa  
 1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu  
 440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg  
 1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg  
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 1545

Thr Leu Gly Glu Val Pro Phe Arg  
 470 475

<210> 970

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 970

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp

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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala	20	25	30
Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val	35	40	45
Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg	50	55	60
Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr	65	70	75
Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu	85	90	95
Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp	100	105	110
Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu	115	120	125
Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu	130	135	140
Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn	145	150	155
Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile	165	170	175
Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val	180	185	190
Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe	195	200	205
Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val	210	215	220
Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr	225	230	235
Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro	245	250	255
Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn	260	265	270
Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala	275	280	285
Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met	290	295	300
Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln	305	310	315
Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile	325	330	335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350

Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser  
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn  
 370 375 380

Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr  
 385 390 395 400

Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu  
 405 410 415

Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln  
 420 425 430

Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala  
 435 440 445

Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr  
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Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg  
 465 470 475

&lt;210&gt; 971

&lt;211&gt; 1191

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1168)

&lt;223&gt; FRXA02281

&lt;400&gt; 971

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 Val Gln Lys Asp Ser  
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
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att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211  
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
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tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc	355
Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg	
70 75 80 85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat	403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	
90 95 100	
tat ccc tgc aag att tac gta tot gag tca gat atc cgc atc cca ccg	451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	
105 110 115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt	499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	
120 125 130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	
135 140 145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	
150 155 160 165	
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	
170 175 180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	
185 190 195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	
200 205 210	
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Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	
215 220 225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	
230 235 240 245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	
250 255 260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	
265 270 275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	
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Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	
295 300 305	

atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att  
1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile  
310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc  
1168

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser  
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1191

<210> 972

<211> 356

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 972

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35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
 195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
 210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240

Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255

Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270

Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285

Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300

Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320

Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
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Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350

Ile Tyr Gly Ser  
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<210> 973  
 <211> 1302  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1279)  
 <223> RXA00147

<400> 973  
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 Val Ser Lys Asp Thr  
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acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163  
 Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu  
 10 15 20

gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc 211  
 Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile  
 25 30 35

ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac 259

Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
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caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
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Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
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Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
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Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
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ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
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Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
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Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
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Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
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Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
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Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
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Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
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Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu	
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Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln	
265 270 275	
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Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly	



280 285 290  
 cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc  
 1027  
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile  
 295 300 305  
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 1075  
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly  
 310 315 320 325  
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 1123  
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys  
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 1171  
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 345 350 355  
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 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala  
 360 365 370  
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 390

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 <211> 393  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 974  
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 35 40 45  
 Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg  
 50 55 60  
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn  
 65 70 75 80  
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu  
 85 90 95

Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr  
 100 105 110  
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly  
 115 120 125  
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile  
 130 135 140  
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu  
 145 150 155 160  
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu  
 165 170 175  
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly  
 180 185 190  
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn  
 195 200 205  
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro  
 210 215 220  
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val  
 225 230 235 240  
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val  
 245 250 255  
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile  
 260 265 270  
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr  
 275 280 285  
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His  
 290 295 300  
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu  
 305 310 315 320  
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile  
 325 330 335  
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu  
 340 345 350  
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala  
 355 360 365  
 Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met  
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 Asp Ala Asp Ala Gln Lys Lys Gly Ala  
 385 390

&lt;210&gt; 975

&lt;211&gt; 1059

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1036)

&lt;223&gt; RXA00145

&lt;400&gt; 975

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                                         Met Lys His Leu Leu
                                         1 5
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Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val Gly Leu Leu Asp Glu
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gcg gat cgc ttt aag gag gtg ctc gaa gga cgt gaa gta aag aag ctg 211
Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg Glu Val Lys Lys Leu
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ccc acg ctg cgt ggt cgc acc att ttt acc ttg ttc tat gag aac tcc 259
Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu Phe Tyr Glu Asn Ser
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Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly Lys Trp Met Ser Ala
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gat gtg att aac att tcg gcc tca tca tcc agc gtg aag aag ggc gag 355
Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser Val Lys Lys Gly Glu
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tcg ctg aaa gat acc ggc ttg act ttg tcg gca atc ggc gcg gat gcg 403
Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala Ile Gly Ala Asp Ala
              90              95              100
atc atc atg cgc cac cca gcc tca ggc gcc gcg cag cag ctt gcg cag 451
Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala Gln Gln Leu Ala Gln
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ttc gtc gca cca ggt ggc aac ggc ccc agc gtg atc aac gcg ggt gac 499
Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val Ile Asn Ala Gly Asp
              120              125              130
ggt tcg cac cag cac ccc acc cag gcg ctt ctc gac gct tta acc atc 547
Gly Ser His Gln His Pro Thr Gln Ala Leu Leu Asp Ala Leu Thr Ile
              135              140              145
cgg cag cgc acc ggc cgc att gag gga ctc aaa gtt gtc atc gtg ggc 595
Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys Val Val Ile Val Gly
              150              155              160              165
gac tgt ttg cac tcc cgg gtg gtg cgc tcc aat gtg gat ctg ctg tcc 643
Asp Cys Leu His Ser Arg Val Val Arg Ser Asn Val Asp Leu Leu Ser
              170              175              180
act ttg ggc gca gag gta gtg ctg gtt gct cct ccg aca ctg ctt cct 691
Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro Pro Thr Leu Leu Pro

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185	190	195	
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Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser Tyr Asp Met Asp Ala			
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gaa att gcc gac gcc gac gta gtg atg atg ctg cgc gtt cag caa gaa			787
Glu Ile Ala Asp Ala Asp Val Val Met Met Leu Arg Val Gln Gln Glu			
215	220	225	
cgc atg cag ggt ggt ttc ttc ccc tca cac cgt gag tac gca acg ctg			835
Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg Glu Tyr Ala Thr Leu			
230	235	240	245
tac ggc atg tcc aaa gag cgc gaa gct cgc ctc aag gac tcc gcc atc			883
Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu Lys Asp Ser Ala Ile			
250	255	260	
atc atg cac ccc ggc ccc atg ctt cgt ggc atg gaa att aac ttc cag			931
Ile Met His Pro Gly Pro Met Leu Arg Gly Met Glu Ile Asn Phe Gln			
265	270	275	
gtg gca gac gca cca cgc acc gcg gta ctg cag cag gta agc aac ggt			979
Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln Gln Val Ser Asn Gly			
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Ala Thr Ile			
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<213> Corynebacterium glutamicum			
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Gly Leu Leu Asp Glu Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg			
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Glu Val Lys Lys Leu Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu			
35	40	45	
Phe Tyr Glu Asn Ser Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly			
50	55	60	
Lys Trp Met Ser Ala Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser			
65	70	75	80
Val Lys Lys Gly Glu Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala			
85	90	95	

Ile Gly Ala Asp Ala Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala  
 100 105 110  
 Gln Gln Leu Ala Gln Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val  
 115 120 125  
 Ile Asn Ala Gly Asp Gly Ser His Gln His Pro Thr Gln Ala Leu Leu  
 130 135 140  
 Asp Ala Leu Thr Ile Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys  
 145 150 155 160  
 Val Val Ile Val Gly Asp Cys Leu His Ser Arg Val Val Arg Ser Asn  
 165 170 175  
 Val Asp Leu Leu Ser Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro  
 180 185 190  
 Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser  
 195 200 205  
 Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu  
 210 215 220  
 Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg  
 225 230 235 240  
 Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu  
 245 250 255  
 Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met  
 260 265 270  
 Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln  
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 Val Ala Gly Ser Asp Ala Thr Ile  
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<210> 977  
 <211> 1464  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1441)  
 <223> RXA00146

<400> 977  
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 Val Val Asp Ser Asn  
 1 5  
 acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca 163

Thr	Gln	Tyr	Pro	Glu	Thr	Gly	Ala	Leu	Ala	Pro	Ala	Pro	Ala	Asp	Ser		
				10					15					20			
ctc	cta	atc	agc	aac	gtt	ttg	gtc	tac	ggc	gaa	ggc	gag	cca	acg	aat	211	
Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu	Gly	Glu	Pro	Thr	Asn		
			25					30					35				
gtg	ttt	gtt	aaa	gat	ggg	gtg	atc	gca	gct	atc	ggc	ggc	act	cat	gag	259	
Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile	Gly	Gly	Thr	His	Glu		
		40					45					50					
gct	gac	cgc	acc	atc	gac	ggc	aat	ggg	gga	gtt	ctc	ctt	cca	ggg	ttc	307	
Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val	Leu	Leu	Pro	Gly	Phe		
	55					60					65						
gtg	gac	atg	cac	gtt	cac	ctg	cgt	gag	cca	ggc	cgc	gaa	gac	act	gaa	355	
Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly	Arg	Glu	Asp	Thr	Glu		
	70				75				80						85		
acc	att	gcc	act	ggg	tct	gcc	gcc	gca	gcc	aag	ggc	gga	ttc	acc	gca	403	
Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys	Gly	Gly	Phe	Thr	Ala		
				90				95						100			
gta	ttc	acc	atg	gcg	aac	acc	act	cca	gtg	atg	gat	cag	ccg	gtt	atc	451	
Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met	Asp	Gln	Pro	Val	Ile		
			105					110					115				
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Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile	Gly	Leu	Cys	Asp	Val		
	120						125					130					
cat	cca	gtt	gga	tcc	atc	acc	aag	ggg	ctt	gag	ggc	aag	gag	ctt	act	547	
His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu	Gly	Lys	Glu	Leu	Thr		
	135					140					145						
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Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys	Val	Arg	Met	Phe	Ser		
	150				155				160						165		
gat	gat	ggc	aag	tgc	gtc	gat	gat	cct	cag	gtc	atg	cgc	cgc	gcg	ctg	643	
Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val	Met	Arg	Arg	Ala	Leu		
				170				175						180			
gaa	tac	gcc	aag	ggc	atg	gac	gtt	ttg	atc	gcc	cag	cac	gct	gag	gat	691	
Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala	Gln	His	Ala	Glu	Asp		
			185					190					195				
cac	cgc	ctg	act	gag	ggc	gct	tca	gca	cac	gag	ggg	gaa	aac	gca	gct	739	
His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu	Gly	Glu	Asn	Ala	Ala		
		200					205					210					
cgt	ctg	ggg	ctg	cgc	ggc	tgg	cca	cgt	gtg	gct	gag	gaa	tcc	atc	gtg	787	
Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala	Glu	Glu	Ser	Ile	Val		
	215					220					225						
gtg	cgc	gat	gcc	atc	atg	gct	cgt	gac	tac	ggc	aac	cgc	gtg	cac	atc	835	
Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly	Asn	Arg	Val	His	Ile		
	230				235				240					245			
tgc	cac	gcc	tcc	act	gaa	ggc	acc	gtg	gag	ttg	ctt	cgt	tgg	gct	aag	883	
Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu	Leu	Arg	Trp	Ala	Lys		

1344

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1464

<210> 978

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 978

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Ala	Pro	Ala	Asp	Ser	Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu
			20					25					30		
Gly	Glu	Pro	Thr	Asn	Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile
		35					40					45			
Gly	Gly	Thr	His	Glu	Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val
	50					55					60				
Leu	Leu	Pro	Gly	Phe	Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly
65					70					75					80
Arg	Glu	Asp	Thr	Glu	Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys
				85					90						95
Gly	Gly	Phe	Thr	Ala	Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met
			100					105					110		
Asp	Gln	Pro	Val	Ile	Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile
		115					120					125			
Gly	Leu	Cys	Asp	Val	His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu
	130					135					140				
Gly	Lys	Glu	Leu	Thr	Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys
145					150					155					160
Val	Arg	Met	Phe	Ser	Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val
				165					170					175	
Met	Arg	Arg	Ala	Leu	Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala
			180					185					190		
Gln	His	Ala	Glu	Asp	His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu
		195					200					205			
Gly	Glu	Asn	Ala	Ala	Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala
	210					215					220				
Glu	Glu	Ser	Ile	Val	Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly
225					230					235					240
Asn	Arg	Val	His	Ile	Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu
			245						250					255	
Leu	Arg	Trp	Ala	Lys	Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr
			260					265					270		



Pro His His Leu Thr Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala  
 275 280 285

Val Asn Lys Val Asn Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala  
 290 295 300

Leu Lys Lys Ala Leu Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp  
 305 310 315 320

His Ala Pro His Gly Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala  
 325 330 335

Lys Pro Gly Met Leu Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp  
 340 345 350

Thr Phe Val Ala Thr Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val  
 355 360 365

Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg  
 370 375 380

Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly  
 385 390 395 400

Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn  
 405 410 415

Thr Pro Phe Glu Gly Gln Glu Phe Ser Ala Lys Val Thr His Thr Val  
 420 425 430

Leu Arg Gly Lys Val Thr Cys Ala Asp Gly Val Ala Gln Asn Ala  
 435 440 445

&lt;210&gt; 979

&lt;211&gt; 1025

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1002)

&lt;223&gt; RXA02208

&lt;400&gt; 979

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 Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys  
 1 5 10 15

atc atc gca gtg cac gat gat tcc ctc tcc cag gaa gtc ttc ggc gtc 96  
 Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val  
 20 25 30

acc ttc cca cga cca cta ggc ctc gcc gca ggt ttc gac aaa aac gca 144  
 Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala  
 35 40 45

tca atg gct gat gcc tgg ggt gcc gtt gga ttc gga tac gcc gaa ctt 192  
 Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu  
 50 55 60

ggc acc gtc acc gcc ttc cca cag cca gga aac ccc acc ccg cgc ctt	240
Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu	
65 70 75 80	
ttc cgc ctg cct gcc gac aaa gct atc ttg aac cgc atg gga ttc aac	288
Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn	
85 90 95	
aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc	336
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser	
100 105 110	
acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct	384
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala	
115 120 125	
gaa cac gca gta gat gac tac cgc cgt tct gca tct ttg tta ggt gat	432
Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp	
130 135 140	
ctt gct gat tac ctg gtt gtc aac gtt tcc tcc ccc aac act ccg ggt	480
Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly	
145 150 155 160	
ctc cgc gat ctg cag gct gtg gaa tct ttg cga cca atc ctc gcc gca	528
Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala	
165 170 175	
gtg cag gaa tcc acc acc gtc cca gtc ttg gtg aaa atc gca cca gac	576
Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp	
180 185 190	
ctc tcc gac gaa gac atc gac gcc gta gct gac ctg gca gtt gag ctc	624
Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu	
195 200 205	
aaa ctc gcc gga atc gta gcc acc aat acc acc att tcc cgc gaa ggc	672
Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly	
210 215 220	
ctc aac act cct tca ggt gaa gtc gaa gcc atg ggt gct ggc gga atc	720
Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile	
225 230 235 240	
tcc ggt gct cca gta gca gcc cga tct ttg gag gta ctc aag cgc ctc	768
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	
245 250 255	
tac gca cgg gta ggc aaa gag atg gtg ttg atc tct gtc ggt ggc atc	816
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	
260 265 270	
agc acc cct gag caa gcc tgg gaa cgc atc acc tcc ggc gca acc ctt	864
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	
275 280 285	
ctg cag gga tac acc cca ttc atc tac ggt ggc ccc gat tgg atc aga	912
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	
290 295 300	
gat atc cac ctt ggt atc gcc aag cag ctg aaa gct cac ggt ctg cgc	960

Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg  
 305 310 315 320

aac atc gct gac gct gtg ggc agc gaa ttg gag tgg aag aac  
 1002

Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn  
 325 330

taaacagacc aaacacacgt gcc  
 1025

<210> 980

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 980

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 20 25 30

Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala  
 35 40 45

Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu  
 50 55 60

Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu  
 65 70 75 80

Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn  
 85 90 95

Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser  
 100 105 110

Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala  
 115 120 125

Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp  
 130 135 140

Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly  
 145 150 155 160

Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala  
 165 170 175

Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp  
 180 185 190

Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu  
 195 200 205

Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly  
 210 215 220

Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile

225	230	235	240
Ser Gly Ala	Pro Val Ala Ala Arg Ser	Leu Glu Val Leu Lys Arg Leu	
	245	250	255
Tyr Ala Arg	Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile		
	260	265	270
Ser Thr Pro	Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu		
	275	280	285
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg			
290	295	300	
Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg			
305	310	315	320
Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn			
	325	330	

&lt;210&gt; 981

&lt;211&gt; 675

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(652)

&lt;223&gt; RXA01660

&lt;400&gt; 981

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                                     Met Ser Ser Asn Ser
                                     1 5
att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta 163
Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu Leu Ile Lys Glu Leu
                        10 15 20
gct gtc gtc cac ggt gaa gtc acc ttg tct tcg ggc aag aag gct gat 211
Ala Val Val His Gly Glu Val Thr Leu Ser Ser Gly Lys Lys Ala Asp
                        25 30 35
tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc 259
Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His Ala Arg Ala Ser Arg
                        40 45 50
ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac 307
Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala Asp Trp Asp Tyr Asp
                        55 60 65
gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc 355
Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro Val Ala Thr Ala Ile
                        70 75 80 85
atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag 403
Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe Val Val Arg Lys Glu
                        90 95 100

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gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg 451  
 Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr  
 105 110 115  
 ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc 499  
 Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser  
 120 125 130  
 cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg 547  
 Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val  
 135 140 145  
 ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc 595  
 Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile  
 150 155 160 165  
 gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt 643  
 Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu Gly Leu Ser Asp Leu  
 170 175 180  
 gga ctc aac taacaccccc ggccccacgg agt 675  
 Gly Leu Asn

&lt;210&gt; 982

&lt;211&gt; 184

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 982

Met Ser Ser Asn Ser Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu  
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 Leu Ile Lys Glu Leu Ala Val Val His Gly Glu Val Thr Leu Ser Ser  
 20 25 30  
 Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His  
 35 40 45  
 Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala  
 50 55 60  
 Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro  
 65 70 75 80  
 Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe  
 85 90 95  
 Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu  
 100 105 110  
 Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr  
 115 120 125  
 Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala  
 130 135 140  
 Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly  
 145 150 155 160

Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu  
 165 170 175

Gly Leu Ser Asp Leu Gly Leu Asn  
 180

<210> 983

<211> 957

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(934)

<223> RXA02235

<400> 983

gtgtcaccgc agctgtccag ggcataagagg ccttgcgtga gggcgttgct agcgtccgcg 60

cgctgcagga actcgaccac gcagtcaagg cttaagccct atg aca ttc ggc gag 115  
 Met Thr Phe Gly Glu  
 1 5

aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att 163  
 Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile  
 10 15 20

gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta 211  
 Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val  
 25 30 35

gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac 259  
 Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp  
 40 45 50

acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt 307  
 Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly  
 55 60 65

tcc gct ggc ttt gcc atc ttg gaa gaa acc att cag acg ctg cgt gag 355  
 Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu  
 70 75 80 85

cgt ggc tgt ttg gtg gtc tct gac gcc aaa cgc ggc gat att ggc tcc 403  
 Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg Gly Asp Ile Gly Ser  
 90 95 100

acc atg gct ggc tat gcc tca gcg tgg tta gat cca gcg tca ccg ctg 451  
 Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu  
 105 110 115

tct agc gac gct gtg acg gtc tct ccc tac ctt ggt ttt cat tcc ttg 499  
 Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu  
 120 125 130

gac cca gtg ttc gaa ctt gcc gag caa cac ggc agg gga gtg ttt gtc 547  
 Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val  
 135 140 145

ttg gcc gcg acc tca aac cct gag gcc cgc gaa ctc cag gac cag caa 595  
 Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln  
 150 155 160 165  
  
 aac gct gac ggc gtg agc att tcc cag cag atc gtg gat cag gca gcg 643  
 Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala  
 170 175 180  
  
 gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc 691  
 Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys Ala Gly Asn Ile Gly  
 185 190 195  
  
 gtc gtc atc ggc gcc acc ttg tcc aaa cca cca cgc tta tcg acg ctc 739  
 Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu  
 200 205 210  
  
 ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca 787  
 Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala  
 215 220 225  
  
 agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835  
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro  
 230 235 240 245  
  
 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883  
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met  
 250 255 260  
  
 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931  
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg  
 265 270 275  
  
 tca tagtcgcgga aacggccctt aat 957  
 Ser

&lt;210&gt; 984

&lt;211&gt; 278

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 984

Met Thr Phe Gly Glu Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg  
 1 5 10 15  
  
 Leu Cys Val Gly Ile Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly  
 20 25 30  
  
 Leu Pro Val Asn Val Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val  
 35 40 45  
  
 Glu Ala Phe Ala Asp Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe  
 50 55 60  
  
 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile  
 65 70 75 80  
  
 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg  
 85 90 95

Gly Asp Ile Gly Ser Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp  
 100 105 110  
 Pro Ala Ser Pro Leu Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu  
 115 120 125  
 Gly Phe His Ser Leu Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly  
 130 135 140  
 Arg Gly Val Phe Val Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu  
 145 150 155 160  
 Leu Gln Asp Gln Gln Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile  
 165 170 175  
 Val Asp Gln Ala Ala Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys  
 180 185 190  
 Ala Gly Asn Ile Gly Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro  
 195 200 205  
 Arg Leu Ser Thr Leu Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala  
 210 215 220  
 Gln Gly Gly Thr Ala Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala  
 225 230 235 240  
 His Leu Ala Phe Pro Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro  
 245 250 255  
 Asp Ile Ala Glu Met Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe  
 260 265 270  
 Pro Gly Phe Pro Arg Ser  
 275

&lt;210&gt; 985

&lt;211&gt; 852

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(829)

&lt;223&gt; RXN01892

&lt;400&gt; 985

ggtctcagtg gcttcttggt tgctgtgatt ttttcaaggc gtaccccggtg gccgatgtta 60  
 aaagcgggttg gcacaacccc tactgaagga gaacaccact gtg acc acc tcg agt 115  
 Val Thr Thr Ser Ser  
 1 5

gaa caa ccc cgt aca gga tac aag cga gtg atg tta aag ctc gga ggt 163  
 Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Gly Gly  
 10 15 20

gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta gac 211  
 Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp  
 25 30 35



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aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag att 259
Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu Ile
      40                      45                      50

gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt cag 307
Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln
      55                      60                      65

cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc ggc 355
Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly
      70                      75                      80                      85

aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat ggc 403
Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly
      90                      95                      100

gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca gaa 451
Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala Glu
      105                      110                      115

cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc gtt 499
Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg Val
      120                      125                      130

gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac acc 547
Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp Thr
      135                      140                      145

act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg atg 595
Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu Met
      150                      155                      160                      165

gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac cca 643
Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn Pro
      170                      175                      180

gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag aag 691
Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu Lys
      185                      190                      195

ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac aac 739
Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp Asn
      200                      205                      210

aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att gct 787
Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile Ala
      215                      220                      225

cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 829
Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser
      230                      235                      240

tgatacattt agtcttataa aca 852

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&lt;210&gt; 986

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 986

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met  
 1 5 10 15  
 Leu Lys Leu Gly Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp  
 20 25 30  
 Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys  
 35 40 45  
 Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg  
 50 55 60  
 Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr  
 65 70 75 80  
 Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe  
 85 90 95  
 Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met  
 100 105 110  
 Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu  
 115 120 125  
 Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr  
 130 135 140  
 Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys  
 145 150 155 160  
 Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp  
 165 170 175  
 Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys  
 180 185 190  
 Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser  
 195 200 205  
 Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr  
 210 215 220  
 Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu  
 225 230 235 240  
 Val Glu Ser

&lt;210&gt; 987

&lt;211&gt; 798

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (47)..(775)

&lt;223&gt; FRXA01892

&lt;400&gt; 987

atgttaaaag cggttggcac aaccctact gaaggagaac accacggtg acc acc tcg 58  
Val Thr Thr Ser  
1

agt gaa caa ccc cgt aca gga tac aaa cga gtg atg tta aag ctc gaa 106  
Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Glu  
5 10 15 20

ggt gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta 154  
Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val  
25 30 35

gac aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag 202  
Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu  
40 45 50

att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250  
Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu  
55 60 65

cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298  
Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu  
70 75 80

ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346  
Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His  
85 90 95 100

ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394  
Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala  
105 110 115

gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442  
Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg  
120 125 130

gtt gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac 490  
Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp  
135 140 145

acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538  
Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu  
150 155 160

atg gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac 586  
Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn  
165 170 175 180

cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634  
Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu  
185 190 195

aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682  
Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp  
200 205 210

aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730  
Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile  
215 220 225

gct cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 775

Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser  
 230 235 240

tgatacattt agtcttataa aca

798

<210> 988

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 988

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met  
 1 5 10 15

Leu Lys Leu Glu Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp  
 20 25 30

Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys  
 35 40 45

Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg  
 50 55 60

Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr  
 65 70 75 80

Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe  
 85 90 95

Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met  
 100 105 110

Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu  
 115 120 125

Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr  
 130 135 140

Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys  
 145 150 155 160

Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp  
 165 170 175

Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys  
 180 185 190

Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser  
 195 200 205

Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr  
 210 215 220

Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu  
 225 230 235 240

Val Glu Ser

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<210> 989
<211> 798
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(775)  
<223> RXA00105
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<400> 989																		
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cgaggagaat ggaacttact aacgctgtta tgatgacggc																		
Met Thr Val Pro Thr																		115
1 5																		
cct tat gaa gac ctt ctt cgg aag att gct gaa gaa ggg tcc cac aag																		163
Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu Glu Gly Ser His Lys																		
10 15 20																		
gac gac cgc acc ggc acc ggc act act tct tta ttc gga caa caa atc																		211
Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu Phe Gly Gln Gln Ile																		
25 30 35																		
cgc ttt gat ctc aat gaa ggt ttt ccc ctt ctg acc acc aag aag gtc																		259
Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu Thr Thr Lys Lys Val																		
40 45 50																		
cat ttc cac tct gtt gtg ggt gag ctt ttg tgg ttc ctt cag ggg gat																		307
His Phe His Ser Val Val Gly Glu Leu Leu Trp Phe Leu Gln Gly Asp																		
55 60 65																		
tcc aac gtc aaa tgg ctg cag gat aac aac atc cgc att tgg aat gaa																		355
Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile Arg Ile Trp Asn Glu																		
70 75 80 85																		
tgg gca gat gag gac ggc gag ctg ggc cct gtt tat ggt gtc cag tgg																		403
Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val Tyr Gly Val Gln Trp																		
90 95 100																		
cgt tct tgg cca acc cct gat ggt cgt cac att gac cag atc tca ggt																		451
Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile Asp Gln Ile Ser Gly																		
105 110 115																		
gct tta gaa act ctg cga aac aac cct gat tca cgt cgc aat att gtc																		499
Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser Arg Arg Asn Ile Val																		
120 125 130																		
tcg gcg tgg aat gtt tcc gag ctt gaa aac atg gct ctt ccc cct tgt																		547
Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met Ala Leu Pro Pro Cys																		
135 140 145																		
cac ttg ctt ttc cag ctc tat gtc gcc gat ggc aaa ctg tct tgc cag																		595
His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly Lys Leu Ser Cys Gln																		
150 155 160 165																		
ctc tac cag cgt tct gcg gac atg ttc ctg ggt gtg cct ttc aac atc																		643
Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly Val Pro Phe Asn Ile																		
170 175 180																		

gca tct tat gca ctg ctc acc cac atg ttt gcc cag cag gca ggc ttg 691  
 Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala Gln Gln Ala Gly Leu  
                   185                                  190                                  195

gaa gtc ggc gag ttc att tgg act ggc ggc gac tgc cac att tat gac 739  
 Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp Cys His Ile Tyr Asp  
                   200                                  205                                  210

aac cac aag gaa cag gtc gcg gag cag ctg agc cga taagctcgcc 785  
 Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser Arg  
                   215                                  220                                  225

cctacccccac ctt 798

<210> 990

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 990

Met Thr Val Pro Thr Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu  
           1                                  5                                  10                                  15

Glu Gly Ser His Lys Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu  
                   20                                  25                                  30

Phe Gly Gln Gln Ile Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu  
                   35                                  40                                  45

Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp  
                   50                                  55                                  60

Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile  
                   65                                  70                                  75                                  80

Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val  
                   85                                  90                                  95

Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile  
                   100                                  105                                  110

Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser  
                   115                                  120                                  125

Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met  
                   130                                  135                                  140

Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly  
                   145                                  150                                  155                                  160

Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly  
                   165                                  170                                  175

Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala  
                   180                                  185                                  190

Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp  
                   195                                  200                                  205

Cys His Ile Tyr Asp Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser

210 215 220

Arg  
225

<210> 991  
<211> 732  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(709)  
<223> RXA00131

<400> 991  
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acgttgcagg cccattcaag ccggagcact accgctacta atg att gtc agc att 115  
Met Ile Val Ser Ile  
1 5

gag gga atc gac ggc gcc ggc aaa aac acc ctg gtt tcg gca tta acg 163  
Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr  
10 15 20

cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211  
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser  
25 30 35

att cac gcc caa ttg gcc gcg gaa gca ctc cac ggc cgc atg ggc gac 259  
Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp  
40 45 50

ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307  
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg  
55 60 65

cac ttc gcg att gat gac tta aat gcg ccc ggc gtg gtg ctg ctc gac 355  
His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp  
70 75 80 85

cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403  
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp  
90 95 100

gac gac gcc ccc cgc tgg gtt gcc gac ctg gaa ttc ggg cgg ctt ggg 451  
Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly  
105 110 115

ctc cca cgt ccg acg ctt caa gtg ttg ttg gat acc ccc gcg gag gta 499  
Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val  
120 125 130

gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547  
Ala Gln Asp Arg Ala Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala  
135 140 145

cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595  
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu

150                      155                      160                      165

cac tat cgc cgc ctc gcg gcg gac aac tgg gaa tca ccg tgg atc gtg      643  
 His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val  
                                  170                                   175                                   180

gtt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa      691  
 Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu  
                                  185                                   190                                   195

ttc ctg ggt act ata aac taatcccaat tagcaggaag gat                      732  
 Phe Leu Gly Thr Ile Asn  
                                  200

&lt;210&gt; 992

&lt;211&gt; 203

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 992

Met Ile Val Ser Ile Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu  
   1                                  5                                  10                                  15

Val Ser Ala Leu Thr Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro  
                                   20                                  25                                  30

Arg Tyr Glu Thr Ser Ile His Ala Gln Leu Ala Ala Glu Ala Leu His  
                                   35                                  40                                  45

Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu  
                                   50                                  55                                  60

Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly  
                                   65                                  70                                  75                                  80

Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala  
                                   85                                  90                                  95

Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu  
                                   100                                  105                                  110

Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp  
                                   115                                  120                                  125

Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu  
                                   130                                  135                                  140

Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln  
                                   145                                  150                                  155                                  160

Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu  
                                   165                                  170                                  175

Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala  
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Gln Arg Ile Val Glu Phe Leu Gly Thr Ile Asn  
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<211> 531
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(508)
<223> RXA00266
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[illegible]

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<210> 994
<211> 136
<212> PRT
<213> Corynebacterium glutamicum
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1	5	10	15
Gly His Val	Gly Glu Ile Ile Ala Arg	Ile Glu Arg Lys	Gly Leu Lys
	20	25	30
Leu Ala Ala	Leu Asp Leu Arg Val Ala Asp Arg	Glu Thr Ala Glu Lys	
	35	40	45
His Tyr Glu	Glu His Ala Asp Lys Pro Phe Phe	Gly Glu Leu Val Glu	
	50	55	60
Phe Ile Thr	Ser Ala Pro Leu Ile Ala Gly Ile Val	Glu Gly Glu Arg	
	65	70	75
Ala Ile Asp	Ala Trp Arg Gln Leu Ala Gly Gly Thr	Asp Pro Val Ala	
	85	90	95
Lys Ala Thr	Pro Gly Thr Ile Arg Gly Asp Phe Ala	Leu Thr Val Gly	
	100	105	110
Glu Asn Val	Val His Gly Ser Asp Ser Pro Glu Ser	Ala Glu Arg Glu	
	115	120	125
Ile Ser Ile	Trp Phe Pro Asn Leu		
	130	135	

&lt;210&gt; 995

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(808)

&lt;223&gt; RXA00718

&lt;400&gt; 995

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actcctctga gctgaccagc ttatacaagg tgggtccaact gtg acg gaa att tcc 115
                                   Val Thr Glu Ile Ser
                                   1                               5
aac atg cct gcc ggt ggc ctc atc gta gcc atc gac ggg ccg tct ggc 163
Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly
                                   10                               15                               20
acc gga aaa tcc acc aca tcc cgc gcg ctc gca acc cgt ctc tcg gcc 211
Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala
                                   25                               30                               35
aag tac cta gat act ggt gcg atg tac cgc gtc gca acg ctt cat gtg 259
Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val
                                   40                               45                               50
ctt aac cag ggg att gac cct gca gat agc gca gcc gtg atc gct gca 307
Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala
                                   55                               60                               65
acc gct gta ttg ccg ttg tcg att tct gac gat ccc gcc tcc act gag 355

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Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp Pro Ala Ser Thr Glu  
 70 75 80 85  
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 Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp Ile Arg Gly Pro Glu  
 90 95 100  
 gtc acc caa aat gtc tcc gca gtg tcc gcg atc cct gag gtt cgt gaa 451  
 Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile Pro Glu Val Arg Glu  
 105 110 115  
 aac ttg gtg gcg ttg cag cgc gca ctc gcc gcc aaa gca cat cgc tgc 499  
 Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala Lys Ala His Arg Cys  
 120 125 130  
 gtc gtc gaa ggc aga gac atc gga acg gca gtg ctt gtc gac gcg ccc 547  
 Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val Leu Val Asp Ala Pro  
 135 140 145  
 atc aag gcg ttt ctc acc gcc tca gcg gaa gtc cgc gcc cag cga cgc 595  
 Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val Arg Ala Gln Arg Arg  
 150 155 160 165  
 ttt gac caa gac acc gca gca ggt cgc gac gta gat ttc gac gct gtg 643  
 Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val Asp Phe Asp Ala Val  
 170 175 180  
 ctg gca gat gtt gtt cgc cgc gat gaa cta gat tcc acc cgt gcc gcc 691  
 Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp Ser Thr Arg Ala Ala  
 185 190 195  
 tca ccg ctg aaa cca gca gat gat gca cac atc gtg gac acc tct gat 739  
 Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile Val Asp Thr Ser Asp  
 200 205 210  
 atg acc atg gat caa gta ctt gat cac ctc atc cac cta gtg gaa gcc 787  
 Met Thr Met Asp Gln Val Leu Asp His Leu Ile His Leu Val Glu Ala  
 215 220 225  
 tcc gct gaa agg agc aac cag tgactgataa acacaccatg cct 831  
 Ser Ala Glu Arg Ser Asn Gln  
 230 235

&lt;210&gt; 996

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 996

Val Thr Glu Ile Ser Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile  
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 Asp Gly Pro Ser Gly Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala  
 20 25 30  
 Thr Arg Leu Ser Ala Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val  
 35 40 45  
 Ala Thr Leu His Val Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala  
 50 55 60

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp  
65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp  
85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile  
100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala  
115 120 125

Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val  
130 135 140

Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val  
145 150 155 160

Arg Ala Gln Arg Arg Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val  
165 170 175

Asp Phe Asp Ala Val Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp  
180 185 190

Ser Thr Arg Ala Ala Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile  
195 200 205

Val Asp Thr Ser Asp Met Thr Met Asp Gln Val Leu Asp His Leu Ile  
210 215 220

His Leu Val Glu Ala Ser Ala Glu Arg Ser Asn Gln  
225 230 235

&lt;210&gt; 997

&lt;211&gt; 1785

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1762)

&lt;223&gt; RXA01599

&lt;400&gt; 997

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tcgatgttta ggttcaacca ggaaggctgt ctcagacatc atg acc tct agt cga 115  
Met Thr Ser Ser Arg  
1 5

aaa gtc cgt ccc acc aaa cac att ttc gtc acc ggt gga gtt gtt tcc 163  
Lys Val Arg Pro Thr Lys His Ile Phe Val Thr Gly Gly Val Val Ser  
10 15 20

tca ctc ggc aaa ggc ctg acc gca gca agc ctt ggt caa ttg ctg att 211  
Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu Gly Gln Leu Leu Ile  
25 30 35

gca cgg gga ctg tcg gtg acc atg cag aag ctg gat cca tac ctc aat 259

Ala	Arg	Gly	Leu	Ser	Val	Thr	Met	Gln	Lys	Leu	Asp	Pro	Tyr	Leu	Asn	
		40					45					50				
gtt	gat	ccg	ggc	acc	atg	aat	cct	ttt	gaa	cac	ggt	gaa	gtc	ttt	gtc	307
Val	Asp	Pro	Gly	Thr	Met	Asn	Pro	Phe	Glu	His	Gly	Glu	Val	Phe	Val	
		55				60					65					
acc	gaa	gac	ggg	gca	gaa	aca	gac	ctg	gat	ttg	ggc	cac	tac	gag	cgt	355
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
	70				75					80					85	
ttc	ctc	gat	cgc	aac	ctg	ggg	ctc	aac	gcc	aat	gtc	acc	acc	ggc	aag	403
Phe	Leu	Asp	Arg	Asn	Leu	Gly	Leu	Asn	Ala	Asn	Val	Thr	Thr	Gly	Lys	
				90					95					100		
gtg	tat	tcc	act	gtg	atc	gcc	aag	gag	cgc	agg	gga	gag	tac	ctg	ggt	451
Val	Tyr	Ser	Thr	Val	Ile	Ala	Lys	Glu	Arg	Arg	Gly	Glu	Tyr	Leu	Gly	
			105					110					115			
aaa	act	gtg	cag	gtc	atc	cca	cac	atc	act	gat	gag	atc	aaa	gct	cgt	499
Lys	Thr	Val	Gln	Val	Ile	Pro	His	Ile	Thr	Asp	Glu	Ile	Lys	Ala	Arg	
		120					125					130				
att	ttg	agc	atg	ggc	gaa	cca	gat	gct	cat	ggt	aac	gcc	cca	gac	gtg	547
Ile	Leu	Ser	Met	Gly	Glu	Pro	Asp	Ala	His	Gly	Asn	Ala	Pro	Asp	Val	
	135					140					145					
gtg	atc	tct	gag	gtc	ggt	ggc	acc	gtc	ggt	gac	att	gaa	tcc	cag	cca	595
Val	Ile	Ser	Glu	Val	Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Gln	Pro	
	150				155					160					165	
ttc	ctt	gaa	gca	gct	cgc	cag	gta	cgc	cat	gaa	att	ggt	cgt	gaa	aac	643
Phe	Leu	Glu	Ala	Ala	Arg	Gln	Val	Arg	His	Glu	Ile	Gly	Arg	Glu	Asn	
			170						175					180		
tgc	ttc	ttc	atc	cac	tgt	tct	ttg	gtg	cca	tac	ttg	gct	acc	tca	ggt	691
Cys	Phe	Phe	Ile	His	Cys	Ser	Leu	Val	Pro	Tyr	Leu	Ala	Thr	Ser	Gly	
			185					190					195			
gag	ctg	aag	acc	aaa	ccc	acc	cag	cat	tct	gtc	gca	gag	ctg	cgc	ggc	739
Glu	Leu	Lys	Thr	Lys	Pro	Thr	Gln	His	Ser	Val	Ala	Glu	Leu	Arg	Gly	
		200					205					210				
atc	ggt	att	ttg	ccg	gat	gct	ctc	gtg	ctt	cgt	tgc	gat	cgg	gag	gtc	787
Ile	Gly	Ile	Leu	Pro	Asp	Ala	Leu	Val	Leu	Arg	Cys	Asp	Arg	Glu	Val	
	215					220					225					
cct	caa	ggt	ctg	aaa	gat	aag	atc	gcg	atg	atg	tgc	gat	gtt	gat	tat	835
Pro	Gln	Gly	Leu	Lys	Asp	Lys	Ile	Ala	Met	Met	Cys	Asp	Val	Asp	Tyr	
	230				235					240					245	
gaa	ggc	gtt	gta	tct	tgc	cct	gat	tcc	agt	tct	att	tac	aac	att	cca	883
Glu	Gly	Val	Val	Ser	Cys	Pro	Asp	Ser	Ser	Ser	Ile	Tyr	Asn	Ile	Pro	
				250					255					260		
gat	gtc	ctc	tac	cgc	gag	cac	ctg	gac	acc	ttc	att	att	cgt	cgc	ctg	931
Asp	Val	Leu	Tyr	Arg	Glu	His	Leu	Asp	Thr	Phe	Ile	Ile	Arg	Arg	Leu	
			265				270						275			
ggc	ctt	ccg	ttc	cgt	gat	gtt	gac	tgg	agc	acc	tgg	cac	gat	ctg	ctg	979
Gly	Leu	Pro	Phe	Arg	Asp	Val	Asp	Trp	Ser	Thr	Trp	His	Asp	Leu	Leu	

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Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly 295 300 305		
aag tac att gat ctt ccc gat gct tat ctc tca gtg gtg gaa gct gtt 1075		
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val 310 315 320 325		
cgc gct gca ggc tac gcc aat tgg acg cgc acc aat atc aag tgg att 1123		
Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile 330 335 340		
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Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala Met Lys Ala Leu Ser 345 350 355		
ggt ttg gat gcc atc gtg gtt ccc gga ggt ttc ggt atc cga ggt atc 1219		
Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe Gly Ile Arg Gly Ile 360 365 370		
gaa ggc aaa atc ggt gcg att acg ttt gca cgt gag cac aag atc ccg 1267		
Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg Glu His Lys Ile Pro 375 380 385		
ctt ctt ggc cta tgc ctt ggc ctg cag tgc acc gtc atc gag gca gca 1315		
Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr Val Ile Glu Ala Ala 390 395 400 405		
cgc cag gca gga ctg gag cag gca tca tcc act gag ttt gac cca gct 1363		
Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr Glu Phe Asp Pro Ala 410 415 420		
gca acg cag cca gtg atc gcc acc atg gaa gag cag aaa gct gct gtg 1411		
Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu Gln Lys Ala Ala Val 425 430 435		
tcg ggt gaa gct gat ctg ggt ggc acc atg cgt ctt ggc gca tat cct 1459		
Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Tyr Pro 440 445 450		
gca acc ctg gag gaa ggc tcc tta gta gcg gaa ctg tat ggc aca acg 1507		
Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu Leu Tyr Gly Thr Thr 455 460 465		
gaa gtc tcc gag cgc cac cgt cac cgc tat gag gtc aat aat gcc tac 1555		
Glu Val Ser Glu Arg His Arg His Arg Tyr Glu Val Asn Asn Ala Tyr 470 475 480 485		

cgc gcc cag att gct gaa ggt tca gat ttg gtc ttc tcc gga acc tca  
1603

Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val Phe Ser Gly Thr Ser  
490 495 500

cct gat gga cat ttg gtg gag ttc gtg gag tac ccc aaa gag gtg cat  
1651

Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr Pro Lys Glu Val His  
505 510 515

cct tat ctg gtg gca acc cag gcg cac cct gag tac aaa tct cgt cca  
1699

Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu Tyr Lys Ser Arg Pro  
520 525 530

acc cat gct cat cca ctg ttt tac ggc ctg gtg aag acc gct ttg gag  
1747

Thr His Ala His Pro Leu Phe Tyr Gly Leu Val Lys Thr Ala Leu Glu  
535 540 545

ctg cgt gtc cac cct tagatctaca atgtgatcat ggt  
1785

Leu Arg Val His Pro  
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<210> 998

<211> 554

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 998

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20 25 30

Gly Gln Leu Leu Ile Ala Arg Gly Leu Ser Val Thr Met Gln Lys Leu  
35 40 45

Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His  
50 55 60

Gly Glu Val Phe Val Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu  
65 70 75 80

Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn  
85 90 95

Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg  
100 105 110

Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp  
115 120 125

Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly  
130 135 140

Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp

145		150		155		160
Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu						
	165			170		175
Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr						
	180			185		190
Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val						
	195			200		205
Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg						
	210			215		220
Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met						
	225			230		235
Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser						
	245			250		255
Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe						
	260			265		270
Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr						
	275			280		285
Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr						
	290			295		300
Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser						
	305			310		315
Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr						
	325			330		335
Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala						
	340			345		350
Met Lys Ala Leu Ser Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe						
	355			360		365
Gly Ile Arg Gly Ile Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg						
	370			375		380
Glu His Lys Ile Pro Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr						
	385			390		395
Val Ile Glu Ala Ala Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr						
	405			410		415
Glu Phe Asp Pro Ala Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu						
	420			425		430
Gln Lys Ala Ala Val Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg						
	435			440		445
Leu Gly Ala Tyr Pro Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu						
	450			455		460
Leu Tyr Gly Thr Thr Glu Val Ser Glu Arg His Arg His Arg Tyr Glu						
	465			470		475
						480



Val Asn Asn Ala Tyr Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val  
 485 490 495

Phe Ser Gly Thr Ser Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr  
 500 505 510

Pro Lys Glu Val His Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu  
 515 520 525

Tyr Lys Ser Arg Pro Thr His Ala His Pro Leu Phe Tyr Gly Leu Val  
 530 535 540

Lys Thr Ala Leu Glu Leu Arg Val His Pro  
 545 550

&lt;210&gt; 999

&lt;211&gt; 3462

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3439)

&lt;223&gt; RXN02234

&lt;400&gt; 999

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tgatggatgc agacgctcag aagaaaggcg cataaataac atg cca aag cgt tca 115  
 Met Pro Lys Arg Ser  
 1 5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163  
 Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly  
 10 15 20

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211  
 Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu  
 25 30 35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259  
 Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr  
 40 45 50

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307  
 Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile  
 55 60 65

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc 355  
 Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly  
 70 75 80 85

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403  
 His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu  
 90 95 100

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc 451  
 Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly  
 105 110 115

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat 499  
 Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp  
 120 125 130

cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547  
 Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala  
 135 140 145

cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca 595  
 Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala  
 150 155 160 165

gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc 643  
 Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly  
 170 175 180

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691  
 Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala  
 185 190 195

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa 739  
 Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu  
 200 205 210

tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc 787  
 Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr  
 215 220 225

gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835  
 Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu  
 230 235 240 245

ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883  
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu  
 250 255 260

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931  
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile  
 265 270 275

cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc 979  
 Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile  
 280 285 290

aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg  
 1027  
 Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val  
 295 300 305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc  
 1075  
 Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala  
 310 315 320 325

aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc  
 1123  
 Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr  
 330 335 340

aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac  
 1171  
 Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp  
 345 350 355

tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc  
 1219  
 Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly  
 360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg  
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 1987  
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 Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp  
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 Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His  
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 Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu  
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 Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala  
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 3427  
 Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His  
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Ala	Cys	Arg	Val	Leu	Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn	35	40	45	
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His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser	165	170	175	
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Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile	Glu	225	230	235	240
Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	Ala	245	250	255	
Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp	Gln				

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Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala	Val				
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Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val	Glu				
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Ser	Ile	Asp	Pro	Trp	Phe	Leu	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gln	Phe				
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Arg	Gln	Lys	Leu	Val	Asp	Ala	Pro	Phe	Leu	Asn	Glu	Asp	Leu	Leu	Arg				
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Glu	Ala	Lys	Phe	Met	Gly	Leu	Ser	Asp	Leu	Gln	Ile	Ala	Ala	Leu	Arg				
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Pro	Glu	Phe	Ala	Gly	Glu	Asp	Gly	Val	Arg	Thr	Leu	Arg	Leu	Ser	Leu				
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 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser  
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 1488

Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu  
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 1536  
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro  
 500 505 510  
 gca gct gag tct gag gtc gca cca cag act gag cgt gaa aag gtc ctg  
 1584  
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu  
 515 520 525  
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 1632  
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp  
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 1680  
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu  
 545 550 555 560  
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 1728  
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 565 570 575  
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 1776  
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 580 585 590  
 gag gtc tac cac gct gag gcg cag tcc ggc acc gtc gca ggt gtt atc  
 1824  
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile  
 595 600 605  
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 1920  
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 1968  
 Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu  
 645 650 655  
 cct gct cca gca ttc ggc acc gca acc tct ttc gaa gag gct cgc aca  
 2016  
 Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr  
 660 665 670  
 gta gcc gat gag atc agc tac cca gtg ctg gtt cgc cct tcc tac gtc  
 2064  
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675	680	685
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Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu 705 710 715 720		
ggt gac cgc ttc cta gac aac gct att gag atc gac gtc gac gca ctg 2208		
Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu 725 730 735		
tgc gac ggc gac gag gtc tac ctg gca ggc gtc atg gag cac atc gag 2256		
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu 740 745 750		
gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg 2304		
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met 755 760 765		
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Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys 770 775 780		
ctg gct ctg ggc atc ggt gta cag ggc ctg atg aac gtc cag tac gca 2400		
Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala 785 790 795 800		
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Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser 805 810 815		
cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag 2496		
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys 820 825 830		
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Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp 850 855 860		
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Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg 865 870 875 880		

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 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys  
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tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat  
 2736  
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr  
 900 905 910

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 2784  
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr  
 915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca  
 2832  
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
 930 935 940

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acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc  
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 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
 965 970 975

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 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
 980 985 990

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 995 1000 1005

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ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc  
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<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 1002

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			20					25					30		
Lys	Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu
	35						40					45			
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Ile	Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr
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			100					105					110		
Val	His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro
			115					120					125		
Ser	Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu
	130					135					140				
Asp	Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala
145					150					155					160
Asn	Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu
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Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile
			180					185					190		
Glu	Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val
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Ala	Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp
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Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys
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Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile
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Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala
			260					265						270	



Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr  
 275 280 285  
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala  
 290 295 300  
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala  
 305 310 315 320  
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys  
 325 330 335  
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu  
 340 345 350  
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr  
 355 360 365  
 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala  
 370 375 380  
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val  
 385 390 395 400  
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala  
 405 410 415  
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln  
 420 425 430  
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu  
 435 440 445  
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu  
 450 455 460  
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser  
 465 470 475 480  
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu  
 485 490 495  
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro  
 500 505 510  
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu  
 515 520 525  
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp  
 530 535 540  
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu  
 545 550 555 560  
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp  
 565 570 575  
 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met  
 580 585 590  
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile

595	600	605
Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys		
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Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met		
625	630	635 640
Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu		
	645	650 655
Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr		
	660	665 670
Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val		
	675	680 685
Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu		
	690	695 700
Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu		
	705	710 715 720
Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu		
	725	730 735
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu		
	740	745 750
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met		
	755	760 765
Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys		
	770	775 780
Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala		
	785	790 795 800
Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser		
	805	810 815
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys		
	820	825 830
Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp		
	835	840 845
Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp		
	850	855 860
Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg		
	865	870 875 880
Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys		
	885	890 895
Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr		
	900	905 910
Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr		
	915	920 925

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
 930 935 940

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
 945 950 955 960

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
 965 970 975

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
 980 985 990

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
 995 1000 1005

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val  
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Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
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Leu Gln Glu Leu Asp His Ala Val Lys Ala  
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 <223> RXN00450

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115  
 Val Gly Val Leu Pro  
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu  
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211  
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val  
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att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259  
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg  
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gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307  
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg  
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr  
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403  
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val  
 90 95 100

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 Gly Ala Arg Ile Gly Arg Ile  
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<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1004

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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
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Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
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 Val Gly Val Leu Pro  
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu

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Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val				
	25	30	35	
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga				259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg				
	40	45	50	
gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga				307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg				
	55	60	65	
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc				355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr				
	70	75	80	85
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg				403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val				
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ggt gct cga atc gga				418
Gly Ala Arg Ile Gly				
	105			

&lt;210&gt; 1006

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1006

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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val				
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Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr				
35	40	45		

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu				
50	55	60		

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg				
65	70	75	80	

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys				
85	90	95		

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly		
100	105	

&lt;210&gt; 1007

&lt;211&gt; 1368

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1345)

&lt;223&gt; RXN02272

&lt;400&gt; 1007

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agttttgaaaa tatgccttga catgtagaaa tggagttctt gtg cgc att aca aac 115  
Val Arg Ile Thr Asn  
1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163  
Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly  
10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211  
Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp  
25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259  
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln  
40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307  
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile  
55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg 355  
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp  
70 75 80 85

gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg 403  
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala  
90 95 100

aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc 451  
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe  
105 110 115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499  
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu  
120 125 130

gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag 547  
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln  
135 140 145

att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag 595  
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln  
150 155 160 165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc 643  
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly  
170 175 180

atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa 691  
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys  
185 190 195

tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac 739  
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His

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gca gaa gcc gca aaa cgt Ala Glu Ala Ala Lys Arg 230	gac atg ggc gca caa acc Asp Met Gly Ala Gln Thr 235	gtg gtg tct cat Val Val Ser His 240	835
tct gtg gcg atg gcc tat Ser Val Ala Met Ala Tyr 250	tac tca cct ggc tac Tyr Ser Pro Gly Tyr 255	atg gcg cga ctt tta Met Ala Arg Leu Leu 260	883
ccc aag ctc gca gca tca Pro Lys Leu Ala Ala Ser 265	aag gtt cgt ttt gca gta Lys Val Arg Phe Ala Val 270	tgc ccc aat gaa Cys Pro Asn Glu 275	931
aac ctc cat ctg caa gga Asn Leu His Leu Gln Gly 280	ctt ggt ttc caa gga Leu Gly Phe Gln Gly 285	ccc gtc ccc cga ggt Pro Val Pro Arg Gly 290	979
gtt gca ccg gta aag caa Val Ala Pro Val Lys Gln 295	ctt acc gaa tgg gga Leu Thr Glu Trp Gly 300	att cca gta agt ttt Ile Pro Val Ser Phe 305	
tgc cag gac tca ctc aat Cys Gln Asp Ser Leu Asn 310	gac ccc ttc tac ccc Asp Pro Phe Tyr Pro 315	atg ggc gat gga gat Met Gly Asp Gly Asp 320	
cta ctc cgc att ctc gat Leu Leu Arg Ile Leu Asp 330	tct gga tta cac gtg Ser Gly Leu His Val 335	tcc cac atg ctc aca Ser His Met Leu Thr 340	
gcc agc cac ttg aag aat Ala Ser His Leu Lys Asn 345	gca cta tcg ttc atc Ala Leu Ser Phe Ile 350	acc acc aat cca gcc Thr Thr Asn Pro Ala 355	
gga aac cta ggc ctg gac Gly Asn Leu Gly Leu Asp 360	aat tac gac att gca Asn Tyr Asp Ile Ala 365	gaa aac tcc ccg gcg Glu Asn Ser Pro Ala 370	
aac ctg ctg gtt ctt gat Asn Leu Leu Val Leu Asp 375	gcg agc agc gag aag Ala Ser Ser Glu Lys 380	gaa gct gta cag aga Glu Ala Val Gln Arg 385	
aaa gct tcc gta ctt ttg Lys Ala Ser Val Leu Leu 390	agc atc cac cgc ggc Ser Ile His Arg Gly 395	aaa aag gtg ctc tcc Lys Lys Lys Val Leu Ser 400	
agg gag ccc gaa cag gtg Arg Glu Pro Glu Gln Val 410	gac tgg aac atc taacagccca Asp Trp Asn Ile 415	gttgggcctc	

ctt  
1368

<210> 1008  
<211> 415  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 1008

Val	Arg	Ile	Thr	Asn	Ala	Gln	Val	Lys	Asn	Tyr	Ala	Glu	Leu	Val	Asp	1	5	10	15
Ile	Thr	Ile	Glu	Gly	Glu	Lys	Ile	Ser	Ser	Ile	Thr	Pro	Ser	Ser	Ile	20	25	30	
Arg	Ser	Glu	Glu	Asp	His	Arg	Ala	Asp	Asp	Tyr	Asp	Ala	Ala	Gly	Arg	35	40	45	
Leu	Val	Ala	Pro	Gln	Phe	Ala	Glu	Ala	His	Ile	His	Leu	Asp	Tyr	Ala	50	55	60	
Asn	Thr	Ala	Gly	Ile	Pro	Arg	Glu	Asn	Ser	Ser	Gly	Thr	Leu	Phe	Glu	65	70	75	80
Ala	Ile	Glu	Ile	Trp	Ala	Asp	Arg	Lys	Thr	Gln	Gly	Phe	His	Ile	Lys	85	90	95	
Glu	Asp	Ile	Lys	Ala	Lys	Ala	Leu	Gln	Ala	Ala	Arg	Arg	Ala	Ala	Glu	100	105	110	
His	Gly	Val	Gly	Phe	Ile	Arg	Thr	His	Val	Asp	Val	Thr	Asp	Pro	Thr	115	120	125	
Phe	Ala	Gly	Phe	Glu	Ala	Ile	Ala	Glu	Leu	Arg	Asp	Glu	Val	Arg	Glu	130	135	140	
Trp	Cys	Asp	Ile	Gln	Ile	Val	Ala	Phe	Pro	Gln	Asn	Gly	Ile	Tyr	Ala	145	150	155	160
Tyr	Glu	Gly	Gly	Gln	Lys	Leu	Ile	Ser	Asp	Ala	Met	Ser	Ala	Gly	Ala	165	170	175	
Asp	Val	Val	Gly	Gly	Ile	Pro	His	Leu	Glu	Pro	Thr	Arg	Asp	Asp	Gly	180	185	190	
Val	Glu	Ser	Val	Lys	Trp	Leu	Phe	Asp	Leu	Ala	Glu	Lys	His	Ser	Ala	195	200	205	
Pro	Ile	Asp	Ile	His	Thr	Asp	Glu	Ile	Asp	Asp	Pro	His	Ser	Arg	Phe	210	215	220	
Val	Glu	Val	Leu	Ala	Ala	Glu	Ala	Ala	Lys	Arg	Asp	Met	Gly	Ala	Gln	225	230	235	240
Thr	Val	Val	Ser	His	Ser	Val	Ala	Met	Ala	Tyr	Tyr	Ser	Pro	Gly	Tyr	245	250	255	
Met	Ala	Arg	Leu	Leu	Pro	Lys	Leu	Ala	Ala	Ser	Lys	Val	Arg	Phe	Ala	260	265	270	



Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly  
 275 280 285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly  
 290 295 300

Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro  
 305 310 315 320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val  
 325 330 335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile  
 340 345 350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala  
 355 360 365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys  
 370 375 380

Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly  
 385 390 395 400

Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile  
 405 410 415

&lt;210&gt; 1009

&lt;211&gt; 1368

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1345)

&lt;223&gt; FRXA02272

&lt;400&gt; 1009

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agtttgaaaa tatgccttga catgtagaaa tggagttctt gtg cgc att aca aac 115  
 Val Arg Ile Thr Asn  
 1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163  
 Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly  
 10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211  
 Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp  
 25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259  
 His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln  
 40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307  
 Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile  
 55' 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg	355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp	
70 75 80 85	
gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg	403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala	
90 95 100	
aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc	451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe	
105 110 115	
atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa	499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu	
120 125 130	
gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag	547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln	
135 140 145	
att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag	595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln	
150 155 160 165	
aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc	643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly	
170 175 180	
atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa	691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys	
185 190 195	
tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac	739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His	
200 205 210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala	
215 220 225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat	835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His	
230 235 240 245	
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta	883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu	
250 255 260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa	931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu	
265 270 275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt	979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly	
280 285 290	
gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt	1027
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe	
295 300 305	

tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat  
1075

Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp  
310 315 320 325

cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca  
1123

Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr  
330 335 340

gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc  
1171

Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala  
345 350 355

gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg  
1219

Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala  
360 365 370

aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga  
1267

Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg  
375 380 385

aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc  
1315

Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser  
390 395 400 405

agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc  
1365

Arg Glu Pro Glu Gln Val Asp Trp Asn Ile  
410 415

ctt  
1368

<210> 1010

<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 1010

Val Arg Ile Thr Asn Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp  
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Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile  
20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg  
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala  
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu  
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys  
85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu  
100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr  
115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu  
130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala  
145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala  
165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly  
180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala  
195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe  
210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln  
225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr  
245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala  
260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly  
275 280 285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly  
290 295 300

Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro  
305 310 315 320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val  
325 330 335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile  
340 345 350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala  
355 360 365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys  
370 375 380

Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly  
385 390 395 400

Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile

405

410

415

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(580)  
 <223> RXN03004

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cgtagggcccaa ccctgaacgc tgaacgctac actgggttgac gtg ctt ctt tca gat 115  
 Val Leu Leu Ser Asp  
 1 5

cgt gac att cgt aaa tca att gac gca ggc gac ttg gga att gaa cct 163  
 Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp Leu Gly Ile Glu Pro  
 10 15 20

ttc gac gct gag ctg att cag ccg tgc agt gtc gat gtc cgc atg gac 211  
 Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val Asp Val Arg Met Asp  
 25 30 35

cgc tac ttc cgg gtt ttc aat aac tct aag tac acc cac att gac cct 259  
 Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr Thr His Ile Asp Pro  
 40 45 50

aag ttg aat cag gat gag ctg acc agc ctt gtt gag gtt gag gac ggc 307  
 Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val Glu Val Glu Asp Gly  
 55 60 65

gag ggc ttt gtg ctg cat ccg ggt gag ttt gtg ctg gcg tcc acg ctg 355  
 Glu Gly Phe Val Leu His Pro Gly Glu Phe Val Leu Ala Ser Thr Leu  
 70 75 80 85

gaa aag ttc act ttg cct gcg cat ctg gct ggt cgt ttg gag ggt aag 403  
 Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly Arg Leu Glu Gly Lys  
 90 95 100

tcg tct ctt ggt cgt ctt ggc ttg ttg acg cac tct act gct ggt ttc 451  
 Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His Ser Thr Ala Gly Phe  
 105 110 115

att gat cct ggt ttt agt ggt tac atc acg ttg gag ttg tcc aat gtg 499  
 Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu Glu Leu Ser Asn Val  
 120 125 130

gct aat ctg ccg atc acg ttg tgg ccg ggt atg aag gtg ggg cag ctg 547  
 Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met Lys Val Gly Gln Leu  
 135 140 145

gct ttg ttc cag atg agt tcc cct gcg gag act 580  
 Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr  
 150 155 160

<210> 1012  
 <211> 160  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1012

Val	Leu	Leu	Ser	Asp	Arg	Asp	Ile	Arg	Lys	Ser	Ile	Asp	Ala	Gly	Asp
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Leu	Gly	Ile	Glu	Pro	Phe	Asp	Ala	Glu	Leu	Ile	Gln	Pro	Ser	Ser	Val
			20					25					30		
Asp	Val	Arg	Met	Asp	Arg	Tyr	Phe	Arg	Val	Phe	Asn	Asn	Ser	Lys	Tyr
		35					40					45			
Thr	His	Ile	Asp	Pro	Lys	Leu	Asn	Gln	Asp	Glu	Leu	Thr	Ser	Leu	Val
	50					55					60				
Glu	Val	Glu	Asp	Gly	Glu	Gly	Phe	Val	Leu	His	Pro	Gly	Glu	Phe	Val
65					70					75					80
Leu	Ala	Ser	Thr	Leu	Glu	Lys	Phe	Thr	Leu	Pro	Ala	His	Leu	Ala	Gly
				85					90					95	
Arg	Leu	Glu	Gly	Lys	Ser	Ser	Leu	Gly	Arg	Leu	Gly	Leu	Leu	Thr	His
			100					105					110		
Ser	Thr	Ala	Gly	Phe	Ile	Asp	Pro	Gly	Phe	Ser	Gly	Tyr	Ile	Thr	Leu
	115						120					125			
Glu	Leu	Ser	Asn	Val	Ala	Asn	Leu	Pro	Ile	Thr	Leu	Trp	Pro	Gly	Met
	130					135					140				
Lys	Val	Gly	Gln	Leu	Ala	Leu	Phe	Gln	Met	Ser	Ser	Pro	Ala	Glu	Thr
145				150						155					160

<210> 1013  
 <211> 225  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(202)

<223> RXN03137

<400> 1013

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cgcgagcag	ctgagccgat	aagctcgccc	ctaccccacc	ttg gag ctc aac aag		115
				Leu Glu Leu Asn Lys		
				1	5	
gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc						163
Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly						
	10		15		20	

tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcgggtgc 212  
 Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val Ala Val  
                   25                                  30

gatttgggca caa 225

<210> 1014

<211> 34

<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

Leu Glu Leu Asn Lys Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp  
       1                  5                  10                  15

Ile Thr Val Ser Gly Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val  
                   20                  25                  30

Ala Val

<210> 1015

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXN03171

<400> 1015

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cggtcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115  
   Met Asp Ile Thr Ile  
   1                  5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
                   10                  15                  20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
                   25                  30                  35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
                   40                  45                  50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
                   55                  60                  65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
       70                  75                  80                  85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403

Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
                                   90                                  95                                  100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
                                   105                                  110                                  115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
                                   120                                  125                                  130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
                                   135                                  140                                  145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
                                   150                                  155                                  160                                  165

gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
                                   170

<210> 1016  
 <211> 171  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1016  
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
                                   20                                  25                                  30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
                                   35                                  40                                  45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
                                   50                                  55                                  60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
                                   65                                  70                                  75                                  80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
                                   85                                  90                                  95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
                                   100                                  105                                  110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
                                   115                                  120                                  125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
                                   130                                  135                                  140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
                                   145                                  150                                  155                                  160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser



165

170

<210> 1017  
 <211> 613  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(613)  
 <223> FRXA02857

<400> 1017  
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 cgggtcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115  
 Met Asp Ile Thr Ile  
 1 5  
 gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20  
 cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
 25 30 35  
 atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50  
 acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65  
 ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85  
 gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100  
 cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115  
 cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130  
 acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145  
 gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165  
 gac gca ttg gcg gaa tct 613

Asp Ala Leu Ala Glu Ser  
170

<210> 1018

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1018

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr  
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser  
165 170

<210> 1019

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXA02771

<400> 1019

gtttgtgata gatcgacacag tcggtaacgt tgttgtaaat acagacctag ccggtatcgg 60

atggaacatg gaccgttggt ccagaagtga ggaataagta gtg agc gaa caa gct 115  
Val Ser Glu Gln Ala  
1 5

cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163  
 Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu Asp Lys Lys Thr Arg  
                   10                                  15                                  20

tat gtg cag gat ttc cca gaa aaa ggt gtg ctt ttt gaa gac ctc acc 211  
 Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr  
                   25                                  30                                  35

ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259  
 Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met  
                   40                                  45                                  50

gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307  
 Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp  
                   55                                  60                                  65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355  
 Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu  
                   70                                  75                                  80                                  85

ggt gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403  
 Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val  
                                   90                                  95                                  100

acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451  
 Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro  
                                   105                                  110                                  115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499  
 Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp  
                   120                                  125                                  130

gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547  
 Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu  
                   135                                  140                                  145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595  
 Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro  
                   150                                  155                                  160                                  165

ggc ctc ggc ggt agg gat aat ctt ggt gat agg ccc gtc att gtg gtc 643  
 Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg Pro Val Ile Val Val  
                                   170                                  175                                  180

aga gat cct cag tagaaggatc gaaagaaagg cgg 678  
 Arg Asp Pro Gln  
                   185

&lt;210&gt; 1020

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1020

Val Ser Glu Gln Ala Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu  
                   1                                  5                                  10                                  15

Asp Lys Lys Thr Arg Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu  
                   20                                  25                                  30

Phe Glu Asp Leu Thr Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala  
 35 40 45  
 Val Val Asp Ala Met Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile  
 50 55 60  
 Ile Gly Gly Leu Asp Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala  
 65 70 75 80  
 Tyr Lys Leu Gly Leu Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu  
 85 90 95  
 Pro Pro Pro Val Val Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala  
 100 105 110  
 Ala Leu Glu Leu Pro Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile  
 115 120 125  
 Val Leu Ile Asp Asp Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala  
 130 135 140  
 Arg Lys Leu Ile Glu Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu  
 145 150 155 160  
 Ala Ile Glu Val Pro Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg  
 165 170 175  
 Pro Val Ile Val Val Arg Asp Pro Gln  
 180 185

&lt;210&gt; 1021

&lt;211&gt; 723

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(700)

&lt;223&gt; RXA01512

&lt;400&gt; 1021

gggtaaaagc gataatggaa gggtggaagt ggtgcggcaa agtggcaagc ttaagatcac 60

tgattgacac ctgaatctac aacacaaggg gaacgcgacg atg agc aac aac gta 115  
 Met Ser Asn Asn Val 5  
 1

gaa atg gcc gac cac aaa gat ctc aat gtt cca gcc aac cca tac ggc 163  
 Glu Met Ala Asp His Lys Asp Leu Asn Val Pro Ala Asn Pro Tyr Gly 20  
 10 15

acc gac att gaa tca gta ttg atc agc gaa gag aag ctc aag cag cgc 211  
 Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu Lys Leu Lys Gln Arg 35  
 25 30

atc gcc gaa atg gcc aag cgc gtc tcc gaa gag ttc aaa gac gcc gaa 259  
 Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu Phe Lys Asp Ala Glu 50  
 40 45

gaa gac ctc atc ctg gtg tgc gtg ctc aag ggc gcg ttc tac ttc ctg 307

Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly Ala Phe Tyr Phe Leu  
 55 60 65  
 gca gat ttc tcc cgc atg ctc gac atc ccc acc cag tcc gag ttc atg 355  
 Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr Gln Ser Glu Phe Met  
 70 75 80 85  
 gcg gtg tcc tct tac gga aac tcc acc tcc tct tca ggc gtg gtg cgc 403  
 Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser Ser Gly Val Val Arg  
 90 95 100  
 atc ctc aag gac ctg gac aag gaa att gaa ggc cgc gac gtt ttg atc 451  
 Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly Arg Asp Val Leu Ile  
 105 110 115  
 gtg gaa gac atc atc gat tcc gga ctg acc ctg tcc tgg ctg atg cgc 499  
 Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu Ser Trp Leu Met Arg  
 120 125 130  
 aac ctg aaa aac cgc aac cct aag tcc ctc aac gtg atc acc ttg ctg 547  
 Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn Val Ile Thr Leu Leu  
 135 140 145  
 cgt aag cca gag cgc ctg acc acc aac atc gac atg ttc gac att gga 595  
 Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp Met Phe Asp Ile Gly  
 150 155 160 165  
 ttt gat att cca aat gag ttt gtt gtg ggc tac gga ctt gat ttc gca 643  
 Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr Gly Leu Asp Phe Ala  
 170 175 180  
 gaa cgc tac cgc gac ctg cca tat gtg ggc acc ctc gag cct cac gtg 691  
 Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr Leu Glu Pro His Val  
 185 190 195  
 tac tcc gac tagtaatcaa aagtgcgaaa gag 723  
 Tyr Ser Asp  
 200

&lt;210&gt; 1022

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1022

Met Ser Asn Asn Val Glu Met Ala Asp His Lys Asp Leu Asn Val Pro  
 1 5 10 15  
 Ala Asn Pro Tyr Gly Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu  
 20 25 30  
 Lys Leu Lys Gln Arg Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu  
 35 40 45  
 Phe Lys Asp Ala Glu Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly  
 50 55 60  
 Ala Phe Tyr Phe Leu Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr  
 65 70 75 80

Gln Ser Glu Phe Met Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser  
                                   85                                  90                                  95

Ser Gly Val Val Arg Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly  
                                   100                                  105                                  110

Arg Asp Val Leu Ile Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu  
                                   115                                  120                                  125

Ser Trp Leu Met Arg Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn  
                                   130                                  135                                  140

Val Ile Thr Leu Leu Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp  
                                   145                                  150                                  155                                  160

Met Phe Asp Ile Gly Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr  
                                   165                                  170                                  175

Gly Leu Asp Phe Ala Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr  
                                   180                                  185                                  190

Leu Glu Pro His Val Tyr Ser Asp  
                                   195                                  200

&lt;210&gt; 1023

&lt;211&gt; 597

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(574)

&lt;223&gt; RXA02031

&lt;400&gt; 1023

tgcttgggcg ttaacgattc tatatatatc tccctagaaa tcaagtgagc attcatctca 60

ttgcagaacg ttgaagcatc attgactagg atatgtagac atg aca gag gaa cgc 115  
   Met Thr Glu Glu Arg  
   1  5

gag att ctg acc tat gag atg ttc gga aca gca atg cgg gag ctg gcc 163  
   Glu Ile Leu Thr Tyr Glu Met Phe Gly Thr Ala Met Arg Glu Leu Ala  
   10  15  20

caa gaa att att gat gac tac cag cca gat tgc gtg ctg tcc att gcg 211  
   Gln Glu Ile Ile Asp Asp Tyr Gln Pro Asp Cys Val Leu Ser Ile Ala  
   25  30  35

cgt ggt ggt ctt cta atc ggt ggc gca ctt ggt tat gcg ctg ggt atc 259  
   Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly Tyr Ala Leu Gly Ile  
   40  45  50

aag aat gta tgc gtg atc aat gtg gag ttc tac acc gat att gga gag 307  
   Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr Thr Asp Ile Gly Glu  
   55  60  65

cac ttg gag gag cca atg atg ctg cct cca act cca aaa gct gtt gat 355  
   His Leu Glu Glu Pro Met Met Leu Pro Pro Thr Pro Lys Ala Val Asp  
   70  75  80  85

ctc tcg gga atg cgt gtg ctc gtc gct gac gat gtc gcg gat acc gga 403  
 Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp Val Ala Asp Thr Gly  
                     90                    95                    100

aag act ctt gag ttg gtc agg gac ttc ctg ggt gac caa gtt gtc gaa 451  
 Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly Asp Gln Val Val Glu  
                     105                    110                    115

gtg cgc act gca gtg atc tat cac aag cca aac agt gtg ttt aag ccg 499  
 Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn Ser Val Phe Lys Pro  
                     120                    125                    130

gag tat gtg tgg cgt gag act gat aag tgg att aac ttc cca tgg tct 547  
 Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile Asn Phe Pro Trp Ser  
                     135                    140                    145

acc ctg cct cca gtg gag cct tct aag taatttttca cccgtgaaag 594  
 Thr Leu Pro Pro Val Glu Pro Ser Lys  
 150                    155

tgc 597

<210> 1024  
 <211> 158  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1024  
 Met Thr Glu Glu Arg Glu Ile Leu Thr Tyr Glu Met Phe Gly Thr Ala  
   1                    5                    10                    15

Met Arg Glu Leu Ala Gln Glu Ile Ile Asp Asp Tyr Gln Pro Asp Cys  
                     20                    25                    30

Val Leu Ser Ile Ala Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly  
                     35                    40                    45

Tyr Ala Leu Gly Ile Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr  
                     50                    55                    60

Thr Asp Ile Gly Glu His Leu Glu Glu Pro Met Met Leu Pro Pro Thr  
                     65                    70                    75                    80

Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp  
                     85                    90                    95

Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly  
                     100                    105                    110

Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn  
                     115                    120                    125

Ser Val Phe Lys Pro Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile  
                     130                    135                    140

Asn Phe Pro Trp Ser Thr Leu Pro Pro Val Glu Pro Ser Lys  
 145                    150                    155





tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc 691  
 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu  
 185 190 195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740  
 Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr  
 200 205 210

gttgaaacca ctg 753

<210> 1026

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1026

Met Ser Glu Asn Leu Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg  
 1 5 10 15

Ile Gln Met Ile Lys Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu  
 20 25 30

Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu  
 35 40 45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val  
 50 55 60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg  
 65 70 75 80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp  
 85 90 95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala  
 100 105 110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala  
 115 120 125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His  
 130 135 140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val  
 145 150 155 160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser  
 165 170 175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser  
 180 185 190

Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu  
 195 200 205

Val Thr  
 210

<210> 1027

<211> 1158  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1135)  
 <223> RXN02772

<400> 1027

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tgagggtccca ggcctcggcg gtagggataa tcttggtgat aggcccgtca ttgtggtcag 60

agatcctcag tagaaggatc gaaagaaaagg cggcaggaaa atg agt ctg gag cgc 115
                               Met Ser Leu Glu Arg
                               1           5

aac aca caa aaa tct tcc atg ggt gtg cga agc atg tca gcc agg ctt 163
Asn Thr Gln Lys Ser Ser Met Gly Val Arg Ser Met Ser Ala Arg Leu
                10                15                20

gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 211
Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
                25                30                35

ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 259
Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
                40                45                50

gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 307
Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
                55                60                65

att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 355
Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
                70                75                80                85

acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 403
Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
                90                95                100

ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 451
Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
                105                110                115

acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 499
Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
                120                125                130

aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 547
Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
                135                140                145

cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 595
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
                150                155                160                165

aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 643
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
                170                175                180

ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 691

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Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala  
 185 190 195

cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 739  
 Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu  
 200 205 210

gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 787  
 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val  
 215 220 225

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 835  
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu  
 230 235 240 245

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 883  
 Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala  
 250 255 260

gaa gtg ctt ggt cga cca aag cac tac tgg tct atc tat caa aag atg 931  
 Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser Ile Tyr Gln Lys Met  
 265 270 275

atc gtt cgc ggt cgt gat ttt gac gat att ttt gat ctt gtt ggc atc 979  
 Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile  
 280 285 290

cgc atc ctg gta gac aac gtg aac aac tgt gta cgc cgc cat cgg tgt  
 1027  
 Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val Arg Arg His Arg Cys  
 295 300 305

cgt gca ctc cct gtt caa tgc tct gcc tgg ccg att caa aga cta tat  
 1075  
 Arg Ala Leu Pro Val Gln Cys Ser Ala Trp Pro Ile Gln Arg Leu Tyr  
 310 315 320 325

ttc agc ccc gcg ctt cgg tgt cta cca atc cct gca cac cac cgt gat  
 1123  
 Phe Ser Pro Ala Leu Arg Cys Leu Pro Ile Pro Ala His His Arg Asp  
 330 335 340

ggg acc tgg cgg taagcctctg gaagttcagg cac  
 1158  
 Gly Thr Trp Arg  
 345

&lt;210&gt; 1028

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1028

Met Ser Leu Glu Arg Asn Thr Gln Lys Ser Ser Met Gly Val Arg Ser  
 1 5 10 15

Met Ser Ala Arg Leu Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr  
 20 25 30

Asn Pro Val Leu Asp Pro Leu Leu Ser Ile His Arg Gln Phe His Pro

35	40	45
Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg		
50	55	60
Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His		
65	70	75
		80
Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr		
	85	90
		95
Thr Leu Val Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr		
100	105	110
Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu		
115	120	125
Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala		
130	135	140
Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro		
145	150	155
		160
Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr		
165	170	175
Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr		
180	185	190
Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val		
195	200	205
Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys		
210	215	220
Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp		
225	230	235
		240
Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu		
245	250	255
Asn Asn Ile Ala Ala Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser		
260	265	270
Ile Tyr Gln Lys Met Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe		
275	280	285
Asp Leu Val Gly Ile Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val		
290	295	300
Arg Arg His Arg Cys Arg Ala Leu Pro Val Gln Cys Ser Ala Trp Pro		
305	310	315
		320
Ile Gln Arg Leu Tyr Phe Ser Pro Ala Leu Arg Cys Leu Pro Ile Pro		
325	330	335
Ala His His Arg Asp Gly Thr Trp Arg		
340	345	

&lt;210&gt; 1029

<211> 903  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(880)  
 <223> FRXA02772

<400> 1029

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cattgtggtc agagatcctc agtagaagga tcgaaagaaa ggcggcagga aaatgagtct 60

ggagcgcaac acacaaaaat cttccatggg tgtgcgaagc atg tca gcc agg ctt 115
                                         Met Ser Ala Arg Leu
                                         1           5

gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 163
Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
                        10                        15                        20

ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 211
Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
                        25                        30                        35

gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 259
Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
                        40                        45                        50

att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 307
Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
                        55                        60                        65

acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 355
Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
                        70                        75                        80                        85

ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 403
Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
                        90                        95                        100

acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 451
Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
                        105                        110                        115

aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 499
Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
                        120                        125                        130

cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 547
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
                        135                        140                        145

aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 595
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
                        150                        155                        160                        165

ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 643
Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala
                        170                        175                        180

cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 691

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Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu  
 185 190 195

gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 739  
 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val  
 200 205 210

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 787  
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu  
 215 220 225

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 835  
 Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala  
 230 235 240 245

gaa gtg ctt ggt cgn ccn aag cac tct ggt ctt tct ttc aaa aga 880  
 Glu Val Leu Gly Arg Pro Lys His Ser Gly Leu Ser Phe Lys Arg  
 250 255 260

tgatcgttcg cggtcgtgat ttt 903

&lt;210&gt; 1030

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1030

Met Ser Ala Arg Leu Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr  
 1 5 10 15

Asn Pro Val Leu Asp Pro Leu Leu Ser Ile His Arg Gln Phe His Pro  
 20 25 30

Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg  
 35 40 45

Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His  
 50 55 60

Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr  
 65 70 75 80

Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr  
 85 90 95

Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu  
 100 105 110

Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala  
 115 120 125

Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro  
 130 135 140

Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr  
 145 150 155 160

Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr  
 165 170 175

Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val  
 180 185 190  
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys  
 195 200 205  
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp  
 210 215 220  
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu  
 225 230 235 240  
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 Ser Phe Lys Arg  
 260

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 <213> Corynebacterium glutamicum

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 Met Ile Val Arg Gly  
 1 5  
 cgt gat ttt gac gat att ttt gat ctt gtt ggc atc cgc ntc ctg gna 163  
 Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile Arg Xaa Leu Xaa  
 10 15 20  
 gac aac gtg aac aac tgg gta cgc cgc cnt cgg tgt cgt gca ctc ccn 211  
 Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg Cys Arg Ala Leu Pro  
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 Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu Tyr Phe Ser Pro Ala  
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 ctt 262  
 Leu

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 <213> Corynebacterium glutamicum

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Cys Arg Ala Leu Pro Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu  
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Tyr Phe Ser Pro Ala Leu  
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<213> Corynebacterium glutamicum

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<222> (101)..(631)

<223> RXA01835

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 Met Asn Thr Ala Ala  
 1 5

tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163  
 Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val  
 10 15 20

agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211  
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp  
 25 30 35

gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259  
 Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val  
 40 45 50

ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307  
 Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg  
 55 60 65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355  
 Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp  
 70 75 80 85

aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403  
 Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser  
 90 95 100

tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451  
 Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met  
 105 110 115

tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499  
 Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg  
 120 125 130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547



Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr  
 135 140 145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595  
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu  
 150 155 160 165

ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641  
 Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala  
 170 175

gcggcgctcga taa 654

&lt;210&gt; 1034

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1034

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 1 5 10 15

Gly Ile Pro Tyr Val Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala  
 20 25 30

Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp  
 35 40 45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala  
 50 55 60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln  
 65 70 75 80

Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu  
 85 90 95

Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys  
 100 105 110

Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu  
 115 120 125

Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp  
 130 135 140

Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu  
 145 150 155 160

Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser  
 165 170 175

Ala

&lt;210&gt; 1035

&lt;211&gt; 1395

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

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                               Met Tyr Pro Tyr Ser
                               1                     5

gac gca gac gct ttt cga cgc cag cct gag cgc gcc aag tcc agc caa 163
Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg Ala Lys Ser Ser Gln
                               10                     15                     20

ctg cgt acc agc gcc gta gac acc cgc agc gcg ttc gcc cgc gac cgg 211
Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala Phe Ala Arg Asp Arg
                               25                     30                     35

gct cgc gtg ctg cat tct gct gct ctt cga cgc ctc gcg gat aaa acc 259
Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg Leu Ala Asp Lys Thr
                               40                     45                     50

caa gtg gtt ggc ccc aat gat ggt gat act ccg cgc acc cgg ctg acg 307
Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro Arg Thr Arg Leu Thr
                               55                     60                     65

cac tct ttg gaa gta gct caa att gca cgg gga atc gga gct gga ctg 355
His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly Ile Gly Ala Gly Leu
                               70                     75                     80                     85

gat ttg gat cct gat ctg tgc gat ctg gca ggg ctg tgc cat gac att 403
Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly Leu Cys His Asp Ile
                               90                     95                     100

ggg cat ccg ccg tat gga cac aac ggt gaa aac gcg ttg aat gaa gtt 451
Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn Ala Leu Asn Glu Val
                               105                     110                     115

gct gcg gcc tgt gga gga ttt gag ggc aac gcc caa acc ttg cgt att 499
Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala Gln Thr Leu Arg Ile
                               120                     125                     130

ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt 547
Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe
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Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala Ala Cys Lys Tyr Pro
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tgg gct aaa aca aat gcg gat ggc agt gtc aat aag aaa tac agt gct 643
Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala
                               170                     175                     180

tat gac gag gac gca gaa atc ctc gct tgg att aga caa ggc cat gag 691
Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu
                               185                     190                     195

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 Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met Asp Phe Ser Asp Asp  
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 Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg  
 215 220 225

atc gac tta aaa gtg ctg tgg gac ctg gtt gaa tta gca gct ttg gca 835  
 Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala  
 230 235 240 245

gac aaa gga gca gct gct ttc gga ggt tcg cct gca gag ctc atc gag 883  
 Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu  
 250 255 260

ggt gca gca tcg ttg cgg gaa ctt ccg gtg gtg gct gcc gct gcg gat 931  
 Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Ala Asp  
 265 270 275

ttt gat ttc tca ctg cgt tcc tac gct gcg ctg aag gcg atg act tca 979  
 Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser  
 280 285 290

gaa cta gtg gga aga tac gtt ggc tct acc atc gag tca aca aag aaa  
 1027  
 Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys  
 295 300 305

aca cac gct ggc att gat gtg gga cgc atg cac ggc gat ttg atc att  
 1075  
 Thr His Ala Gly Ile Asp Val Gly Arg Met His Gly Asp Leu Ile Ile  
 310 315 320 325

cca gaa aca gcg gcc agt gaa gta aaa ctg ctc aaa acg tta gcg gtt  
 1123  
 Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu Lys Thr Leu Ala Val  
 330 335 340

ctc tac gtg atg gat gac cca ggg cac ctt gcg cgc caa aac agg caa  
 1171  
 Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala Arg Gln Asn Arg Gln  
 345 350 355

cgg gat cgt atc ttc cgg gtt ttt gac tac ctg gtg ctg ggg gct ccg  
 1219  
 Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu Val Leu Gly Ala Pro  
 360 365 370

gga tcg ttg gat ccg atg tat cgc cag tgg ttt att gaa gcg gat tca  
 1267  
 Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe Ile Glu Ala Asp Ser  
 375 380 385

gaa tcg gaa cag atc cgt gtg att gtt gat cag att gcg tcg atg acg  
 1315  
 Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr  
 390 395 400 405

gag tct cgt ctg gaa cgc ctt gcc cgg aat gct gct gac atc tca gga  
 1363

Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala Ala Asp Ile Ser Gly  
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 Phe Leu Gly

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<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 1036

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 20 25 30

Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg  
 35 40 45

Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro  
 50 55 60

Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly  
 65 70 75 80

Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly  
 85 90 95

Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn  
 100 105 110

Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala  
 115 120 125

Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp  
 130 135 140

Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala  
 145 150 155 160

Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn  
 165 170 175

Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile  
 180 185 190

Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met  
 195 200 205

Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly  
 210 215 220

Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu  
 225 230 235 240

Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro

245										250					255				
Ala	Glu	Leu	Ile	Glu	Gly	Ala	Ala	Ser	Leu	Arg	Glu	Leu	Pro	Val	Val				
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Ala	Ala	Ala	Ala	Asp	Phe	Asp	Phe	Ser	Leu	Arg	Ser	Tyr	Ala	Ala	Leu				
			275				280					285							
Lys	Ala	Met	Thr	Ser	Glu	Leu	Val	Gly	Arg	Tyr	Val	Gly	Ser	Thr	Ile				
		290				295					300								
Glu	Ser	Thr	Lys	Lys	Thr	His	Ala	Gly	Ile	Asp	Val	Gly	Arg	Met	His				
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Gly	Asp	Leu	Ile	Ile	Pro	Glu	Thr	Ala	Ala	Ser	Glu	Val	Lys	Leu	Leu				
			325					330					335						
Lys	Thr	Leu	Ala	Val	Leu	Tyr	Val	Met	Asp	Asp	Pro	Gly	His	Leu	Ala				
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Arg	Gln	Asn	Arg	Gln	Arg	Asp	Arg	Ile	Phe	Arg	Val	Phe	Asp	Tyr	Leu				
		355					360					365							
Val	Leu	Gly	Ala	Pro	Gly	Ser	Leu	Asp	Pro	Met	Tyr	Arg	Gln	Trp	Phe				
		370				375					380								
Ile	Glu	Ala	Asp	Ser	Glu	Ser	Glu	Gln	Ile	Arg	Val	Ile	Val	Asp	Gln				
385					390					395					400				
Ile	Ala	Ser	Met	Thr	Glu	Ser	Arg	Leu	Glu	Arg	Leu	Ala	Arg	Asn	Ala				
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Ala	Asp	Ile	Ser	Gly	Phe	Leu	Gly												
			420																

&lt;210&gt; 1037

&lt;211&gt; 1131

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1108)

&lt;223&gt; RXN01027

&lt;400&gt; 1037

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				Met	Ala	Asn	Lys	Asn	
				1				5	

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Asn	Lys	Pro	His	Glu	Val	Asp	Lys	Asp	Gln	Asp	Ser	Ala	Met	Leu	Ile	
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Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro	Thr	Glu	Glu	Phe	Thr	
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Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr	
40 45 50	
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Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp	
55 60 65	
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Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro	
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aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt	403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg	
90 95 100	
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc	451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr	
105 110 115	
aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc	499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val	
120 125 130	
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca	547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala	
135 140 145	
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Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala	
150 155 160 165	
gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc	643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg	
170 175 180	
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag	691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys	
185 190 195	
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc	739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro	
200 205 210	
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Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr Ser Ala Val Pro Asp	
215 220 225	
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Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp	
230 235 240 245	
gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc	883
Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro	
250 255 260	
gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg	931
Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val	
265 270 275	
ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg	979

Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp  
 280 285 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa  
 1027

Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys  
 295 300 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc  
 1075

Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly  
 310 315 320 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg ttttaaggcct  
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Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 330 335

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 1131

<210> 1038

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 1038

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Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp  
 35 40 45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His  
 50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro  
 65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr  
 85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro  
 100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu  
 115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu  
 130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu  
 145 150 155 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg  
 165 170 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly  
 180 185 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala  
 195 200 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr  
 210 215 220

Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp  
 225 230 235 240

Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala  
 245 250 255

Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val  
 260 265 270

Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro  
 275 280 285

Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu  
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Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp  
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 <213> Corynebacterium glutamicum

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 <223> FRXA01024

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 Met Ala Asn Lys Asn  
 1 5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163  
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile  
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211  
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr  
 25 30 35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259  
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr



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Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp			
55	60	65	
gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg			355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro			
70	75	80	85
aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt			403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg			
	90	95	100
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc			451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr			
	105	110	115
aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc			499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val			
	120	125	130
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca			547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala			
	135	140	145
tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca			595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala			
	150	155	160
gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc			643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg			
	170	175	180
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag			691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys			
	185	190	195
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc			739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro			
	200	205	210
atg ttg ttg ccc ttc aaa			757
Met Leu Leu Pro Phe Lys			
215			

&lt;210&gt; 1040

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1040

Met	Ala	Asn	Lys	Asn	Lys	Pro	His	Glu	Val	Asp	Lys	Asp	Gln	Asp
1				5				10					15	

Ser	Ala	Met	Leu	Ile	Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro
			20					25					30		

Thr	Glu	Glu	Phe	Thr	Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp
	35						40					45			

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His  
 50 55 60  
 Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro  
 65 70 75 80  
 Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr  
 85 90 95  
 Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro  
 100 105 110  
 Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu  
 115 120 125  
 Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu  
 130 135 140  
 Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu  
 145 150 155 160  
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg  
 165 170 175  
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly  
 180 185 190  
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala  
 195 200 205  
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys  
 210 215

&lt;210&gt; 1041

&lt;211&gt; 257

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(234)

&lt;223&gt; FRXA01027

&lt;400&gt; 1041

acc gat ccc gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa 48  
 Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln  
 1 5 10 15

ggt ggc gtg ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg 96  
 Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met  
 20 25 30

atc aaa tgg ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc 144  
 Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile  
 35 40 45

aag gcg aaa aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg 192  
 Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val  
 50 55 60

ttc acc ggc gct gat tac ctg gcg agt tcc ctg ccg gtt aaa 234  
 Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 65 70 75

taggagcgcg tttaaggcct cca 257

<210> 1042

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 1042

Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln  
 1 5 10 15

Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met  
 20 25 30

Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile  
 35 40 45

Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val  
 50 55 60

Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 65 70 75

<210> 1043

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01528

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gggtcgtagg tctccaacca ggaggcggtc caacacgagg gtg aat cag gcg tgg 115  
 Val Asn Gln Ala Trp  
 1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163  
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu  
 10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211  
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp  
 25 30 35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259  
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly  
 40 45 50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307  
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp

55	60	65	
aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac			355
Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His			
70	75	80	85
ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg			403
Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser			
90	95		100
gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat			451
Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr			
105	110		115
gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg			499
Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala			
120	125		130
tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag			547
Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu			
135	140		145
cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg			595
Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu			
150	155	160	165
aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaacccg			648
Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg			
170	175		

aac 651

<210> 1044

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1044

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Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
20 25 30

Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
35 40 45

Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
50 55 60

Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
65 70 75 80

Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
85 90 95

Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
100 105 110

His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu

115	120	125
Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu		
130	135	140
Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu		
145	150	155
Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg		
165	170	175

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 <211> 541  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(541)  
 <223> RXA00072

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 aagaatctct cgaaagacac aaaagaggtg agtcgcaaca atg agc ttt caa cta 115  
 Met Ser Phe Gln Leu  
 1 5  
 gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163  
 Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser  
 10 15 20  
 ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211  
 Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys  
 25 30 35  
 cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259  
 His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala  
 40 45 50  
 agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307  
 Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala  
 55 60 65  
 att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355  
 Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala  
 70 75 80 85  
 gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403  
 Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr  
 90 95 100  
 cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451  
 His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr  
 105 110 115  
 tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499

Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln  
 120 125 130

gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg 541  
 Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala  
 135 140 145

<210> 1046

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 1046

Met Ser Phe Gln Leu Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys  
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Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser  
 20 25 30

Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala  
 35 40 45

Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu  
 50 55 60

His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val  
 65 70 75 80

Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe  
 85 90 95

Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln  
 100 105 110

Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu  
 115 120 125

Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser  
 130 135 140

Asn Pro Ala  
 145

<210> 1047

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(979)

<223> RXA01878

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atagtagaaa tctggcatcc aataggtaga ttgggatgct atg gaa gaa ccc tca 115  
 Met Glu Glu Pro Ser  
 1 5

ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag	163
Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys	
10 15 20	
ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat	211
Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp	
25 30 35	
ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac	259
Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn	
40 45 50	
gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc	307
Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala	
55 60 65	
ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt	355
Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg	
70 75 80 85	
ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt	403
Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu	
90 95 100	
gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa	451
Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln	
105 110 115	
tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac	499
Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr	
120 125 130	
aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc	547
Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr	
135 140 145	
atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg	595
Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu	
150 155 160 165	
gct gcg gat cca gga tgc aag att tat ggt gtg cct agc gtg aag gcg	643
Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala	
170 175 180	
tcc ttc tac ggt cca gtt act cgc gcc ggg tgc att ggt aag aat gtc	691
Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val	
185 190 195	
ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc	739
Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg	
200 205 210	
gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg	787
Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp	
215 220 225	
ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct	835
Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala	
230 235 240 245	

gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883  
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu  
                   250                                  255                                  260

cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931  
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val  
                   265                                  270                                  275

act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979  
 Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys  
                   280                                  285                                  290

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<210> 1048

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

Met Glu Glu Pro Ser Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg  
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Ala Leu Ala Glu Lys Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln  
                   20                                  25                                  30

Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala  
                   35                                  40                                  45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly  
                   50                                  55                                  60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val  
                   65                                  70                                  75                                  80

Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp  
                   85                                  90                                  95

Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala  
                   100                                  105                                  110

Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val  
                   115                                  120                                  125

Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met  
                   130                                  135                                  140

Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu  
                   145                                  150                                  155                                  160

Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val  
                   165                                  170                                  175

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser  
                   180                                  185                                  190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu  
                   195                                  200                                  205



Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr  
 210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg  
 225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala  
 245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly  
 260 265 270

Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln  
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Gln Lys Asp Glu Lys  
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<210> 1049  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(1531)  
 <223> RXN02281

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 Val Gln Lys Asp Ser  
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211  
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355  
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg  
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403  
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn  
 90 95 100

tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg 451

Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro		
			105					110					115				
gag	tac	att	cgc	ggc	gca	cct	tcc	gct	acc	gaa	gct	cgc	cgt	gct	ggt	499	
Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly		
		120					125					130					
gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547	
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp		
		135				140						145					
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg	595	
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro		
150					155				160						165		
ctt	ttc	cac	ttc	ggg	ccg	caa	cgc	ttc	gac	atc	gcc	tgc	gcc	cgc	atc	643	
Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile		
			170					175						180			
gag	cac	tac	acc	ggc	atc	aac	gtg	gaa	cac	gtg	cag	aag	tac	att	ctg	691	
Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu		
			185				190						195				
ttc	acc	aac	tac	gcc	atg	cac	acc	acc	gag	ttc	gtg	cat	ttt	gcc	atg	739	
Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met		
		200					205					210					
tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggt	cta	tcc	ttg	cca	787	
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro		
		215				220					225						
aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggt	acg	gaa	835	
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu		
230					235				240						245		
acc	ctt	gat	ctg	act	agc	cgt	ttc	caa	atg	cct	cgt	tac	gat	ctc	atc	883	
Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile		
				250				255						260			
acc	gaa	gcc	ggt	gac	ggt	att	acc	att	atc	aac	atc	ggt	gtg	ggc	cca	931	
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro		
			265				270						275				
tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa	979	
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu		
		280					285					290					
gcc	tgg	gtg	atg	atc	ggc	cac	tgt	gct	ggc	atg	gac	gcc	cgc	atg	cgc		
1027																	
Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg		
		295				300					305						
atc	ggc	gac	ctc	atc	ctt	ggc	aac	gcc	tac	cag	cgc	gaa	gac	cac	att		
1075																	
Ile	Gly	Asp	Leu	Ile	Leu	Gly	Asn	Ala	Tyr	Gln	Arg	Glu	Asp	His	Ile		
310					315				320					325			
ctg	aat	acc	cgc	atc	cca	ctt	ggt	aat	ccg	atc	ccg	gca	ata	cca	gaa		
1123																	
Leu	Asn	Thr	Arg	Ile	Pro	Leu	Gly	Asn	Pro	Ile	Pro	Ala	Ile	Pro	Glu		
				330				335						340			

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac  
1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp  
345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac  
1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn  
360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc  
1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser  
375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga  
1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly  
390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg  
1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu  
410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac  
1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr  
425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa  
1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu  
440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg  
1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg  
455 460 465

acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga  
1545

Thr Leu Gly Glu Val Pro Phe Arg  
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<210> 1050

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

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Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val  
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
 50 55 60  
 Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
 65 70 75 80  
 Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
 85 90 95  
 Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
 100 105 110  
 Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
 115 120 125  
 Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
 130 135 140  
 Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
 145 150 155 160  
 Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
 165 170 175  
 Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
 180 185 190  
 Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
 195 200 205  
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
 210 215 220  
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240  
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255  
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270  
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285  
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300  
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320  
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
 325 330 335  
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350  
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser  
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn  
 370 375 380  
 Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr  
 385 390 395 400  
 Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu  
 405 410 415  
 Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln  
 420 425 430  
 Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala  
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 Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg  
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 <223> FRXA02281

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 Val Gln Lys Asp Ser  
 1 5  
 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
 10 15 20  
 att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211  
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35  
 aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50  
 gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
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 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg  
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 gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403  
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn

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gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp 135 140 145			547
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro 150 155 160 165			595
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile 170 175 180			643
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu 185 190 195			691
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met 200 205 210			739
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro 215 220 225			787
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu 230 235 240 245			835
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acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro 265 270 275			931
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu 280 285 290			979
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc 1027 Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg 295 300 305			
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att 1075 Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile 310 315 320 325			

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
 1123  
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
                   330                  335                  340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc  
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<210> 1052

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 1052

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Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val  
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Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
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Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
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Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
                   85                  90                  95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
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Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
                   115                  120                  125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
                   130                  135                  140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
   145                  150                  155                  160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
                   165                  170                  175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
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Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
                   195                  200                  205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
                   210                  215                  220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240  
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255  
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270  
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285  
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300  
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320  
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
 325 330 335  
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350  
 Ile Tyr Gly Ser  
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&lt;210&gt; 1053

&lt;211&gt; 1146

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1123)

&lt;223&gt; RXN01240

&lt;400&gt; 1053

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 Met Ser Asp Asn Thr  
 1 5  
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 Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe Arg Arg Ala His Pro  
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 Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu Glu Leu Leu Thr Asp  
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 ggt ggt gtc acc ttc gat cgc gtc acc aca cgc atc aaa gaa tgg tca 259  
 Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser  
 40 45 50  
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 Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile  
 55 60 65



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Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile	
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acc acg tac cac tcc acg gaa ata ccc gtg gcc cta aaa gtg ctc caa	403
Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln	
90 95 100	
gac tcc ttc atc gtc cac aaa tcc gta gac aaa gcc gct gaa act cgc	451
Asp Ser Phe Ile Val His Lys Ser Val Asp Lys Ala Ala Glu Thr Arg	
105 110 115	
atc tca ggc ggc ttt ggt tac ggc tcc cac cac ctg att ctg gaa gtc	499
Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His Leu Ile Leu Glu Val	
120 125 130	
gat gac acc tcc gat gac ctc cag gac tac aaa ggc ctc gtc ttt gaa	547
Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys Gly Leu Val Phe Glu	
135 140 145	
gtt cag gtg cgc acc gtg ctg caa cac gcc tgg gca gag ttc gaa cac	595
Val Gln Val Arg Thr Val Leu Gln His Ala Trp Ala Glu Phe Glu His	
150 155 160 165	
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Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn Pro Glu Asp Phe Ser	
170 175 180	
gca gaa gta gac cgc atg ttc acc ctc gct gcc gga ctc atc gaa tta	691
Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala Gly Leu Ile Glu Leu	
185 190 195	
gcg gac caa caa ttc gac caa atc gcc gca ctc aaa gaa acc agc cga	739
Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu Lys Glu Thr Ser Arg	
200 205 210	
gtt gct gat gaa tcc gtc gaa ctc acc gca gag aca ctt ccc ggc gtt	787
Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val	
215 220 225	
ctt gcc atg ctc att ggc aac cgc ttc ccc cgc cca cgc tcc aca aac	835
Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn	
230 235 240 245	
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Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val	
250 255 260	
gtg cag ctg cgc gag ctg ctc aac ccc acc gac att gaa gtg ctg ttg	931
Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp Ile Glu Val Leu Leu	
265 270 275	
aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac	979
Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp	
280 285 290	
gat tta cta ctc aaa cga ttt ggc caa tca cac atc gat gcc acc gtc	1027
Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His Ile Asp Ala Thr Val	
295 300 305	

gcc acc gac tcc caa cca ctc aac gcc aaa cgc cac agg cag cta aaa  
1075

Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys  
310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac  
1123

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330 335 340

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1146

<210> 1054

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

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Glu Leu Leu Thr Asp Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg  
35 40 45

Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn  
50 55 60

Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met  
65 70 75 80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala  
85 90 95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys  
100 105 110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His  
115 120 125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys  
130 135 140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp  
145 150 155 160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn  
165 170 175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala  
180 185 190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu  
195 200 205

Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu

210	215	220
Thr Leu Pro Gly Val	Leu Ala Met Leu Ile	Gly Asn Arg Phe Pro Arg
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Pro Arg Ser Thr	Asn Tyr Arg Phe Leu Glu Asp	Ile Leu Val Ala Asn
	245	250 255
Ser Ile Thr Ser	Val Val Gln Leu Arg Glu Leu Leu Asn	Pro Thr Asp
	260	265 270
Ile Glu Val Leu Leu Lys Val	Met Asn Tyr Arg Phe His	Pro Gly Gln
	275	280 285
Ile Arg Ile Ile Asp Asp	Leu Leu Leu Lys Arg Phe Gly Gln	Ser His
	290	295 300
Ile Asp Ala Thr Val Ala Thr Asp	Ser Gln Pro Leu Asn Ala Lys Arg	
	305	310 315 320
His Arg Gln Leu Lys Arg Lys Leu Glu Leu Met Thr Gln Ala His Leu		
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Val Glu Pro Pro Asn		
	340	

&lt;210&gt; 1055

&lt;211&gt; 1234

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1234)

&lt;223&gt; RXN02008

&lt;400&gt; 1055

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                               Val Tyr Ala Ala Ile
                               1 5

ggt gtc gtg cac tcc ctg ttc aat gct ctg cct ggc cga ttc aaa gac 163
Gly Val Val His Ser Leu Phe Asn Ala Leu Pro Gly Arg Phe Lys Asp
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Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln Ser Leu His Thr Thr
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Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val Gln Ala Arg Thr His
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gac atg cac tac aac gcc gaa ttc ggc att gca gcg cac tgg cga tac 307
Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala Ala His Trp Arg Tyr
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Pro	Asn	Glu	Phe	Leu	Asp	Ser	Leu	Arg	Tyr	Asp	Leu	Thr	Ser	Lys	Gln		
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Ser	Thr	Pro	Val	Asp	Phe	Ala	Tyr	Ala	Val	His	Thr	Glu	Val	Gly	His		
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Lys	Leu	Lys	Ser	Gly	Asp	Arg	Val	Glu	Val	Phe	Thr	Ser	Lys	Asp	Gln		
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Asn	Ala	Gly	Pro	Ser	Arg	Gly	Trp	Gln	Glu	Phe	Val	Val	Ser	Pro	Arg		
			185					190					195				
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		200					205					210					
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Tyr	Leu	Glu	Ala	Gly	Arg	Asp	Ala	Leu	Ala	Ala	Val	Ile	Gln	Arg	Gly		
		215				220					225						
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Gly	Ser	Gly	Ser	Val	Ser	Ala	Gln	His	Val	Val	Asn	Arg	Leu	Met	Ala		
			265					270					275				
atc	ttt	ggc	gac	gaa	gaa	gat	gcc	gaa	gac	gca	ttg	gtt	gca	cgc	acc	979	
Ile	Phe	Gly	Asp	Glu	Glu	Asp	Ala	Glu	Asp	Ala	Leu	Val	Ala	Arg	Thr		
		280					285					290					
cca	ttc	agc	gag	ctg	gtc	aac	tcc	cgt	gcc	acc	acg	gaa	agc	agc	acc	1027	
Pro	Phe	Ser	Glu	Leu	Val	Asn	Ser	Arg	Ala	Thr	Thr	Glu	Ser	Ser	Thr		
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1075

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1123

Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe Gly Phe Val Thr Arg  
330 335 340

ggg ggc ggt gtc tcc gta cac cga aca gac tgc acg aat gtg gaa aag  
1171

Gly Gly Gly Val Ser Val His Arg Thr Asp Cys Thr Asn Val Glu Lys  
345 350 355

ctc aaa gaa gag cca gaa cgc att gtc tcc gtc tcc tgg gct tcg gaa  
1219

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1234

Gly Gln Gly Ser Val  
375

<210> 1056

<211> 378

<212> PRT

<213> Corynebacterium glutamicum

<400> 1056

Val Tyr Ala Ala Ile Gly Val Val His Ser Leu Phe Asn Ala Leu Pro  
1 5 10 15

Gly Arg Phe Lys Asp Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln  
20 25 30

Ser Leu His Thr Thr Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val  
35 40 45

Gln Ala Arg Thr His Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala  
50 55 60

Ala His Trp Arg Tyr Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln  
65 70 75 80

Ala Glu Val Asp Gln Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln  
85 90 95

Lys Glu Ala Ala Asp Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp  
100 105 110

Leu Thr Ser Lys Gln Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val  
115 120 125

Asn Leu Pro Val Asn Ser Thr Pro Val Asp Phe Ala Tyr Ala Val His  
130 135 140

Thr Glu Val Gly His Arg Cys Ile Gly Ala Lys Ile Asn Gly Lys Leu  
145 150 155 160

Val Ala Leu Glu Thr Lys Leu Lys Ser Gly Asp Arg Val Glu Val Phe  
 165 170 175  
 Thr Ser Lys Asp Gln Asn Ala Gly Pro Ser Arg Gly Trp Gln Glu Phe  
 180 185 190  
 Val Val Ser Pro Arg Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys  
 195 200 205  
 Glu Arg Arg Glu Glu Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala  
 210 215 220  
 Val Ile Gln Arg Gly Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser  
 225 230 235 240  
 Ser Met Lys Thr Val Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala  
 245 250 255  
 Leu Tyr Thr Ala Ile Gly Ser Gly Ser Val Ser Ala Gln His Val Val  
 260 265 270  
 Asn Arg Leu Met Ala Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala  
 275 280 285  
 Leu Val Ala Arg Thr Pro Phe Ser Glu Leu Val Asn Ser Arg Ala Thr  
 290 295 300  
 Thr Glu Ser Ser Thr Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met  
 305 310 315 320  
 Ala Lys Leu Ala Lys Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe  
 325 330 335  
 Gly Phe Val Thr Arg Gly Gly Gly Val Ser Val His Arg Thr Asp Cys  
 340 345 350  
 Thr Asn Val Glu Lys Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val  
 355 360 365  
 Ser Trp Ala Ser Glu Gly Gln Gly Ser Val  
 370 375

&lt;210&gt; 1057

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1036)

&lt;223&gt; RXN01940

&lt;400&gt; 1057

ccagaatcaa tcaccgatac agtggcagcc aaagtccagg ctgaagaagc cgctcaagcc 60

gccagctaaa tccacaaact gaactaagga gttttaccct atg acc acc aag atc 115  
 Met Thr Thr Lys Ile

1

5

atc ctc gac tgc gat cca gga cac gac gac gct gta gcc atg ctg ctc	163
Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu	
10 15 20	
gca gcc ggc agc cca gaa att gaa ctg ctt gga atc acc acg gtc ggc	211
Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly	
25 30 35	
ggc aac cag acc ttg gac aag gtc acc cac aat acg cag gtc gta gcc	259
Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala	
40 45 50	
acc atc gct gat atc aat gcg ccc atc tac cgc ggt gtc acc cga cca	307
Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro	
55 60 65	
ttg gtg cgc ccc gtt gag gta gcc gaa gat atc cac ggc gat acc ggc	355
Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly	
70 75 80 85	
atg gaa atc cac aag tac gaa ctg cct gaa cca acc aag cag gta gaa	403
Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu	
90 95 100	
gac acc cac gcg gtg gat ttc atc atc gat acc atc atg aat aac gag	451
Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr Ile Met Asn Asn Glu	
105 110 115	
ccc ggc agc gta gcg ctg gtt ccc acc gga cca ctg acc aac atc gcg	499
Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro Leu Thr Asn Ile Ala	
120 125 130	
ctg gca gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt	547
Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val	
135 140 145	
gtc ctc atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct	595
Val Leu Met Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala	
150 155 160 165	
gaa ttc aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac	643
Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn	
170 175 180	
gaa aag tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg	691
Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala	
185 190 195	
ctc gca aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac	739
Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp	
200 205 210	
gtc gcc gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac	787
Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr	
215 220 225	
cag gac gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct	835
Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala	
230 235 240 245	
gtt gca tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca	883

Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro  
 250 255 260  
 ctc gat gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct 931  
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala  
 265 270 275  
 gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979  
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val  
 280 285 290  
 gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag  
 1027  
 Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys  
 295 300 305  
 cgc atc gga tagacctgtt cacaagggtg tta  
 1059  
 Arg Ile Gly  
 310  
 <210> 1058  
 <211> 312  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 1058  
 Met Thr Thr Lys Ile Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala  
 1 5 10 15  
 Val Ala Met Leu Leu Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly  
 20 25 30  
 Ile Thr Thr Val Gly Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn  
 35 40 45  
 Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg  
 50 55 60  
 Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile  
 65 70 75 80  
 His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro  
 85 90 95  
 Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr  
 100 105 110  
 Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro  
 115 120 125  
 Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu  
 130 135 140  
 Arg Val Lys Glu Val Val Leu Met Gly Gly Gly Tyr His Val Gly Asn  
 145 150 155 160  
 Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala  
 165 170 175



His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp  
 180 185 190  
 Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn  
 195 200 205  
 Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala  
 210 215 220  
 Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val  
 225 230 235 240  
 His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr  
 245 250 255  
 Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr  
 260 265 270  
 Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr  
 275 280 285  
 Thr Gln Val Ala Val Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val  
 290 295 300  
 Ile Asp Ala Val Lys Arg Ile Gly  
 305 310

&lt;210&gt; 1059

&lt;211&gt; 602

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(579)

&lt;223&gt; FRXA01940

&lt;400&gt; 1059

aga gta acg ctt gtt tcc acc ggg cca ctg acc aac atc gcg ctg gca 48  
 Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala  
 1 5 10 15

gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt gtc ctc 96  
 Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu  
 20 25 30

atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc 144  
 Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe  
 35 40 45

aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag 192  
 Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys  
 50 55 60

tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca 240  
 Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala  
 65 70 75 80

aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac gtc gcc 288  
 Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala

	85	90	95	
gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac cag gac				336
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp				
	100	105	110	
gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct gtt gca				384
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala				
	115	120	125	
tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca ctc gat				432
Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp				
	130	135	140	
gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct gat ttc				480
Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe				
	145	150	155	160
cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt gac ctg				528
Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu				
	165	170	175	
gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag cgc atc				576
Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile				
	180	185	190	
gga tagacctgtt cacaagggtt tta				602
Gly				

&lt;210&gt; 1060

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1060

Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala			
1	5	10	15
Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu			
20	25	30	
Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe			
35	40	45	
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys			
50	55	60	
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala			
65	70	75	80
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala			
85	90	95	
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp			
100	105	110	
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala			
115	120	125	

Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp  
 130 135 140  
 Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe  
 145 150 155 160  
 Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu  
 165 170 175  
 Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile  
 180 185 190

Gly

<210> 1061  
 <211> 1026  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1003)  
 <223> RXA02559

<400> 1061  
 ttagtcctct atggcagcaa gcctgccaga ggagcctatc cagcactaga ccccaactag 60  
 aacccaaccc caaaaccaga aaacactaag ctcgtgagac atg att cct gtt ctc 115  
 Met Ile Pro Val Leu  
 1 5  
 atc gac tgc gac acc ggc atc gac gac gcc ctc gcc ctg atc tac ctg 163  
 Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu  
 10 15 20  
 gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211  
 Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr  
 25 30 35  
 acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259  
 Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala Ile Asn Thr Arg Trp  
 40 45 50  
 gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307  
 Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln  
 55 60 65  
 cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355  
 Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly  
 70 75 80 85  
 gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403  
 Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu  
 90 95 100  
 ggt gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451  
 Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr  
 105 110 115

aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499  
Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro  
120 125 130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547  
Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn  
135 140 145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595  
Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala  
150 155 160 165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643  
Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu  
170 175 180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691  
Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu  
185 190 195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739  
Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met  
200 205 210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787  
Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu  
215 220 225

gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835  
Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile  
230 235 240 245

cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883  
Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro  
250 255 260

ttg atg cgt ggc acc act gtt gca gat att cgc gga cat tgg ggc aag 931  
Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys  
265 270 275

cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979  
Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His  
280 285 290

gcg gaa ctt cta aga gca gtg gaa tgaaataatc cgggtgctgat gca  
1026  
Ala Glu Leu Leu Arg Ala Val Glu  
295 300

&lt;210&gt; 1062

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1062

Met Ile Pro Val Leu Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu  
1 5 10 15

Ala Leu Ile Tyr Leu Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu  
20 25 30

Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala  
 35 40 45  
 Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro  
 50 55 60  
 Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr  
 65 70 75 80  
 Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His  
 85 90 95  
 Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu  
 100 105 110  
 Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu  
 115 120 125  
 Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr  
 130 135 140  
 Leu Tyr Pro Gly Asn Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val  
 145 150 155 160  
 Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile  
 165 170 175  
 Thr Val Cys Ser Leu Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp  
 180 185 190  
 Ile Leu Ser Thr Leu Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu  
 195 200 205  
 His Leu Pro Glu Met Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln  
 210 215 220  
 Gly Glu Gly Tyr Leu Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile  
 225 230 235 240  
 Ala Leu Asp Lys Ile Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val  
 245 250 255  
 Glu Ala Asp Ser Pro Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg  
 260 265 270  
 Gly His Trp Gly Lys Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp  
 275 280 285  
 Ile Glu Ala Ala His Ala Glu Leu Leu Arg Ala Val Glu  
 290 295 300

&lt;210&gt; 1063

&lt;211&gt; 1050

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1027)

&lt;223&gt; RXA02497

&lt;400&gt; 1063

tcgatgccgc cgctggcgaa gactcgggga aacctaataaa taccgaagaa gaatttgacc 60

gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115  
Val Arg Leu Gly Val  
1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163  
Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg  
10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211  
Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg  
25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259  
Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile  
40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307  
Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr  
55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355  
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser  
70 75 80 85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403  
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly  
90 95 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451  
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe  
105 110 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499  
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn  
120 125 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547  
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu  
135 140 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595  
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr  
150 155 160 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643  
His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu  
170 175 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691  
Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met  
185 190 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739  
Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe  
200 205 210

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787  
 Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro  
 215 220 225  
 cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835  
 His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala  
 230 235 240 245  
 ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883  
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile  
 250 255 260  
 agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931  
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu  
 265 270 275  
 gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979  
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp  
 280 285 290  
 gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag  
 1027  
 Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu  
 295 300 305  
 taacatttac ccggaagga gtt  
 1050

&lt;210&gt; 1064

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1064

Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val  
 1 5 10 15  
 Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp  
 20 25 30  
 Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile  
 35 40 45  
 Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala  
 50 55 60  
 Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr  
 65 70 75 80  
 Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val  
 85 90 95  
 Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu  
 100 105 110  
 Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala  
 115 120 125  
 Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser  
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly  
 145 150 155 160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg  
 165 170 175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu  
 180 185 190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly  
 195 200 205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro  
 210 215 220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu  
 225 230 235 240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala  
 245 250 255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly  
 260 265 270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val  
 275 280 285

Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile  
 290 295 300

Asp Lys Gly Leu Glu  
 305

&lt;210&gt; 1065

&lt;211&gt; 2226

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2203)

&lt;223&gt; RXN01079

&lt;400&gt; 1065

accttaaaac ttaatcaatc aatacaaagt tcacacctct tttgaaaggg acattccttt 60

gactgcatcg ggaaccaccg tcgtgccacg cggagaccag atg gac ttc cac gct 115  
 Met Asp Phe His Ala  
 1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163  
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe  
 10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211  
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn  
 25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259



Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu	
40 45 50	
gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc	307
Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe	
55 60 65	
cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc	355
Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg	
70 75 80 85	
ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg	403
Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu	
90 95 100	
aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc	451
Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val	
105 110 115	
tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag	499
Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu	
120 125 130	
aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca	547
Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro	
135 140 145	
acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc	595
Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys	
150 155 160 165	
ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc	643
Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile	
170 175 180	
aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg	691
Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu	
185 190 195	
ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa aac	739
Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Asn	
200 205 210	
cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc	787
Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe	
215 220 225	
tcc tac gct aac cag ctg ggt gct cgt cag ggt gca ggt gct gtg tac	835
Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly Ala Gly Ala Val Tyr	
230 235 240 245	
ctc aac gct cac cac cca gat atc ctg tcc ttc ctg gat acc aag cgt	883
Leu Asn Ala His His Pro Asp Ile Leu Ser Phe Leu Asp Thr Lys Arg	
250 255 260	
gag aac gcc gat gag aag atc cgc atc aag acc ctg tcc ctg ggt gtt	931
Glu Asn Ala Asp Glu Lys Ile Arg Ile Lys Thr Leu Ser Leu Gly Val	
265 270 275	
gtg att ccg gac atc acc ttc gag ctg gct aag cgc aac gat gac atg	979
Val Ile Pro Asp Ile Thr Phe Glu Leu Ala Lys Arg Asn Asp Asp Met	

280	285	290
tac ctg ttc tcc cca tac gat gtg gag cgc att tac ggc aag cct ttc 1027		
Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile Tyr Gly Lys Pro Phe 295 300 305		
gca gac gtc tca atc acc gag cac tac gac gag atg gtg gat gat gac 1075		
Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu Met Val Asp Asp Asp 310 315 320 325		
cgc atc cgc aag acc aag atc aac gcg cgt cag ttc ttc cag acc ctg 1123		
Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln Phe Phe Gln Thr Leu 330 335 340		
gca gaa atc cag ttc gag tcc ggt tac cca tac atc atg tat gaa gac 1171		
Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr Ile Met Tyr Glu Asp 345 350 355		
acc gtg aat gca tcc aac cca atc gaa ggt cgc atc acc cac tca aac 1219		
Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg Ile Thr His Ser Asn 360 365 370		
ctg tgc tct gag atc ctt cag gtg tcc acc cca tct gaa ttc aac gat 1267		
Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro Ser Glu Phe Asn Asp 375 380 385		
gac ctg act tac gca gag gtc ggc gaa gac att tct tgt aac ttg ggt 1315		
Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile Ser Cys Asn Leu Gly 390 395 400 405		
tcc ctc aac gtt gca atg gct atg gat gca cca aac ttt gag aag acc 1363		
Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr 410 415 420		
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc 1411		
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser 425 430 435		
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc 1459		
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala 440 445 450		
atc ggc ctt ggc cag atg aac ctt cac ggc tac ttc ggt cgc gag cac 1507		
Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His 455 460 465		
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt 1555		
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe 470 475 480 485		

gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act  
1603

Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr  
490 495 500

gag cgt gga gag cgt ttc aag aac ttc gaa aac tcc aag tat gca acc  
1651

Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr  
505 510 515

ggt gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc  
1699

Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser  
520 525 530

gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc  
1747

Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr  
535 540 545

gtt gag gac tgg gct gcg ctg aag gcc gac gtg atg gag cac ggt ctg  
1795

Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu  
550 555 560 565

ttc aac cgt aac ctg caa gcg gtt cca cca acc ggt tcg atc tcc tac  
1843

Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr  
570 575 580

atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag  
1891

Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu  
585 590 595

atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac  
1939

Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His  
600 605 610

atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc  
1987

Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly  
615 620 625

tac gag aag atc att gac acc tac gct gtg gca acc aag tac gtt gac  
2035

Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp  
630 635 640 645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt  
2083

Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp Thr Ala Thr Thr Arg  
650 655 660

gac atc aac cgt gcg cag atc tac gca tgg cgc aag ggc atc aag acc  
2131

Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg Lys Gly Ile Lys Thr  
665 670 675

ttg tac tac att cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt  
 2179  
 Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu Glu Gly Thr Glu Val  
           680                                685                                690

gac ggc tgc gtc agc tgc atg ctg taaaagcact taaaaatatc ccc  
 2226  
 Asp Gly Cys Val Ser Cys Met Leu  
           695                                700

<210> 1066

<211> 701

<212> PRT

<213> Corynebacterium glutamicum

<400> 1066

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn  
       1                                5                                10                                15

Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe  
                                 20                                25                                30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu  
                                 35                                40                                45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu  
           50                                55                                60

Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr  
       65                                70                                75                                80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr  
                                 85                                90                                95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg  
                                 100                                105                                110

Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp  
           115                                120                                125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe  
       130                                135                                140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly  
       145                                150                                155                                160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser  
                                 165                                170                                175

Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly  
           180                                185                                190

Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile  
           195                                200                                205

Lys Lys Ile Glu Asn Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu  
       210                                215                                220

Leu Glu Asp Ala Phe Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly  
       225                                230                                235                                240

Ala Gly Ala Val Tyr Leu Asn Ala His His Pro Asp Ile Leu Ser Phe  
 245 250 255  
 Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile Lys Thr  
 260 265 270  
 Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu Ala Lys  
 275 280 285  
 Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile  
 290 295 300  
 Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu  
 305 310 315 320  
 Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln  
 325 330 335  
 Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr  
 340 345 350  
 Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg  
 355 360 365  
 Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro  
 370 375 380  
 Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile  
 385 390 395 400  
 Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro  
 405 410 415  
 Asn Phe Glu Lys Thr Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val  
 420 425 430  
 Pro Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn  
 435 440 445  
 Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr  
 450 455 460  
 Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe  
 465 470 475 480  
 Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser  
 485 490 495  
 Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn  
 500 505 510  
 Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp  
 515 520 525  
 Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn  
 530 535 540  
 Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val  
 545 550 555 560

Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr  
 565 570 575

Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile  
 580 585 590

Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr  
 595 600 605

Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp  
 610 615 620

Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala  
 625 630 635 640

Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp  
 645 650 655

Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg  
 660 665 670

Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu  
 675 680 685

Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu  
 690 695 700

&lt;210&gt; 1067

&lt;211&gt; 790

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(790)

&lt;223&gt; FRXA01079

&lt;400&gt; 1067

accttaaaac ttaatcaatc aatacaaagt tcacacctct tttgaaaggg acatttccttt 60

gactgcatcg ggaaccaccg tcgtgccacg cggagaccag atg gac ttc cac gct 115  
 Met Asp Phe His Ala  
 1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163  
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe  
 10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211  
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn  
 25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259  
 Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu  
 40 45 50

gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc 307  
 Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe  
 55 60 65

cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355  
 Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg  
 70 75 80 85  
  
 ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403  
 Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu  
 90 95 100  
  
 aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451  
 Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val  
 105 110 115  
  
 tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499  
 Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu  
 120 125 130  
  
 aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547  
 Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro  
 135 140 145  
  
 acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595  
 Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys  
 150 155 160 165  
  
 ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc 643  
 Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile  
 170 175 180  
  
 aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg 691  
 Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu  
 185 190 195  
  
 ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa atc 739  
 Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Ile  
 200 205 210  
  
 cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc 787  
 Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe  
 215 220 225  
  
 tcc 790  
 Ser  
 230

&lt;210&gt; 1068

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1068

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn  
 1 5 10 15

Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe  
 20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu  
 35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu

50	55	60
Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr		
65	70	75 80
Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr		
	85	90 95
Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg		
	100	105 110
Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp		
	115	120 125
Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe		
	130	135 140
Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly		
	145	150 155 160
Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser		
	165	170 175
Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly		
	180	185 190
Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile		
	195	200 205
Lys Lys Ile Glu Ile Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu		
	210	215 220
Leu Glu Asp Ala Phe Ser		
225	230	

&lt;210&gt; 1069

&lt;211&gt; 1364

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1341)

&lt;223&gt; FRXA01084

&lt;400&gt; 1069

tcc ttt ctg gat acc aag cgc gag aac gcc gat gag aag atc cgc atc	48
Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile	
1 5 10 15	

aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg	96
Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu	
20 25 30	

gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag	144
Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu	
35 40 45	

cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac	192
Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr	



50	55	60	
gac gag atg gtg gat gat gac cgc atc cgc aag acc aag atc aac gcg Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala 65 70 75 80			240
cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr 85 90 95			288
cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu 100 105 110			336
ggg cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser 115 120 125			384
acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu 130 135 140			432
gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp 145 150 155 160			480
gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr 165 170 175			528
gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys 180 185 190			576
ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His 195 200 205			624
ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu 210 215 220			672
gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg 225 230 235 240			720
gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe 245 250 255			768
gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala 260 265 270			816
aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys 275 280 285			864
tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala 290 295 300			912

gac gtg atg gag cac ggt ctg ttc aac cgt aac ctg caa gcg gtt cca 960  
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro  
 305 310 315 320

cca acc ggt tcg atc tcc tac atc aac aac tcc acc tcg tcg atc cac  
 1008

Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His  
 325 330 335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc  
 1056

Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg  
 340 345 350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc  
 1104

Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe  
 355 360 365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct  
 1152

Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala  
 370 375 380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc  
 1200

Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe  
 385 390 395 400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca  
 1248

Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala  
 405 410 415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt  
 1296

Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val  
 420 425 430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg  
 1341

Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu  
 435 440 445

taaaagcact taaaaatata ccc  
 1364

<210> 1070

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 1070

Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile  
 1 5 10 15

Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu  
 20 25 30

Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu  
                   35                                  40                                  45

Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr  
                   50                                  55                                  60

Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala  
                   65                                  70                                  75                                  80

Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr  
                                   85                                  90                                  95

Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu  
                                   100                                  105                                  110

Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser  
                   115                                  120                                  125

Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu  
                   130                                  135                                  140

Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp  
                   145                                  150                                  155                                  160

Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr  
                                   165                                  170                                  175

Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys  
                                   180                                  185                                  190

Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His  
                   195                                  200                                  205

Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu  
                   210                                  215                                  220

Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg  
                   225                                  230                                  235                                  240

Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe  
                                   245                                  250                                  255

Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala  
                   260                                  265                                  270

Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys  
                   275                                  280                                  285

Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala  
                   290                                  295                                  300

Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro  
                   305                                  310                                  315                                  320

Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His  
                                   325                                  330                                  335

Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg  
                   340                                  345                                  350

Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe

355	360	365
Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala 370	375	380
Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe 385	390	395 400
Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala 405	410	415
Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val 420	425	430
Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu 435	440	445

&lt;210&gt; 1071

&lt;211&gt; 1125

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1102)

&lt;223&gt; RXN01920

&lt;400&gt; 1071

cttctgaagg gcttcggttg gggtaagctg gcgatctgaa atcgcgctgc attgtggcgt 60

cgaaaagcaa aaaaatttgt agaagggaag agcgcaccta atg gct gct gat tct	115
Met Ala Ala Asp Ser	
1 5	

gat ctc agt gtt cac gat gct tac tta aag gag cat gtt gca cct gta	163
Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu His Val Ala Pro Val	
10 15 20	

aag gcg atc aac tgg aac tcc atc cca gat tcc aaa gat ctt gaa gtc	211
Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser Lys Asp Leu Glu Val	
25 30 35	

tgg gat cgt ctg acc ggt aac ttc tgg ctc cca gaa aag gtc cca gta	259
Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro Glu Lys Val Pro Val	
40 45 50	

tcc aac gac atc aag agc tgg gga acc ctc aac gag gtt gaa aaa gcc	307
Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn Glu Val Glu Lys Ala	
55 60 65	

gca acc atg cgc gtg ttc acc gga ctt acc ctg ctg gac acc att cag	355
Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu Leu Asp Thr Ile Gln	
70 75 80 85	

ggc act gtc ggc gca atc tcc ctg ctt cca gac gca gat tca ctg cac	403
Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp Ala Asp Ser Leu His	
90 95 100	

gaa gaa gcg gtg cta acc aac att gcg ttc atg gaa tcc gtg cac gca	451
Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met Glu Ser Val His Ala	

105										110					115					
aag	agt	tac	tcc	aac	atc	ttc	atg	act	ctg	gcc	tcc	acc	gcg	gaa	atc	499				
Lys	Ser	Tyr	Ser	Asn	Ile	Phe	Met	Thr	Leu	Ala	Ser	Thr	Ala	Glu	Ile					
		120							125				130							
aac	gat	gcg	ttc	cgt	tgg	tct	gag	gaa	aat	gaa	aac	ctg	cag	cgc	aag	547				
Asn	Asp	Ala	Phe	Arg	Trp	Ser	Glu	Glu	Asn	Glu	Asn	Leu	Gln	Arg	Lys					
		135				140						145								
gca	aag	atc	atc	ctg	tct	tac	tat	gag	ggc	gat	gat	cca	cta	aag	cgc	595				
Ala	Lys	Ile	Ile	Leu	Ser	Tyr	Tyr	Glu	Gly	Asp	Asp	Pro	Leu	Lys	Arg					
		150				155				160					165					
aag	atc	gcc	tcc	gtg	atc	ctg	gag	tcc	ttc	ctg	ttc	tac	tcc	ggc	ttc	643				
Lys	Ile	Ala	Ser	Val	Ile	Leu	Glu	Ser	Phe	Leu	Phe	Tyr	Ser	Gly	Phe					
				170					175					180						
tac	ctc	cca	atg	tat	tgg	tcc	agc	cac	tcc	aag	ctg	gcc	aac	acc	gcc	691				
Tyr	Leu	Pro	Met	Tyr	Trp	Ser	Ser	His	Ser	Lys	Leu	Ala	Asn	Thr	Ala					
			185					190					195							
gac	gtg	atc	cgc	ctg	atc	atc	cgc	gat	gag	gca	gtg	cac	ggc	tac	tac	739				
Asp	Val	Ile	Arg	Leu	Ile	Ile	Arg	Asp	Glu	Ala	Val	His	Gly	Tyr	Tyr					
		200					205					210								
att	ggc	tac	aag	tat	caa	aag	gct	gtc	gcg	aag	gag	act	cca	gag	cgt	787				
Ile	Gly	Tyr	Lys	Tyr	Gln	Lys	Ala	Val	Ala	Lys	Glu	Thr	Pro	Glu	Arg					
		215				220					225									
cag	gaa	gag	ctg	aag	gag	tac	acc	ttc	gat	ctg	ctc	tac	gat	ctt	tac	835				
Gln	Glu	Glu	Leu	Lys	Glu	Tyr	Thr	Phe	Asp	Leu	Leu	Tyr	Asp	Leu	Tyr					
		230				235				240					245					
gat	aac	gaa	act	cag	tac	tcc	gaa	gat	ctc	tac	gac	gat	ctt	gga	tgg	883				
Asp	Asn	Glu	Thr	Gln	Tyr	Ser	Glu	Asp	Leu	Tyr	Asp	Asp	Leu	Gly	Trp					
				250					255					260						
acc	gag	gat	gtt	aag	cga	ttc	ctt	cgc	tac	aac	gcc	aac	aag	gcc	ctc	931				
Thr	Glu	Asp	Val	Lys	Arg	Phe	Leu	Arg	Tyr	Asn	Ala	Asn	Lys	Ala	Leu					
			265					270					275							
aac	aac	ctt	ggc	tac	gaa	gga	ctc	ttc	cca	gcg	gat	gaa	acc	aag	gtg	979				
Asn	Asn	Leu	Gly	Tyr	Glu	Gly	Leu	Phe	Pro	Ala	Asp	Glu	Thr	Lys	Val					
		280					285					290								
tcc	cca	aac	atc	ttg	tct	gcg	ctg	tca	cca	aac	gct	gat	gag	aac	cac					
																1027				
Ser	Pro	Asn	Ile	Leu	Ser	Ala	Leu	Ser	Pro	Asn	Ala	Asp	Glu	Asn	His					
		295				300						305								
gac	ttc	ttc	tcc	ggc	tcc	ggt	tcc	tct	tac	gtt	att	ggt	aag	gca	gaa					
																1075				
Asp	Phe	Phe	Ser	Gly	Ser	Gly	Ser	Ser	Tyr	Val	Ile	Gly	Lys	Ala	Glu					
					315					320					325					
aac	acc	gag	gat	gat	gac	tgg	gac	ttc	taacttttaa	aaagctgaag										
																1122				
Asn	Thr	Glu	Asp	Asp	Asp	Trp	Asp	Phe												
																330				

cgc  
1125

<210> 1072

<211> 334

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1072

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Met Ala Ala Asp Ser Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu
  1             5             10             15

His Val Ala Pro Val Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser
      20             25             30

Lys Asp Leu Glu Val Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro
      35             40             45

Glu Lys Val Pro Val Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn
      50             55             60

Glu Val Glu Lys Ala Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu
      65             70             75             80

Leu Asp Thr Ile Gln Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp
      85             90             95

Ala Asp Ser Leu His Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met
      100            105            110

Glu Ser Val His Ala Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala
      115            120            125

Ser Thr Ala Glu Ile Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu
      130            135            140

Asn Leu Gln Arg Lys Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp
      145            150            155            160

Asp Pro Leu Lys Arg Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu
      165            170            175

Phe Tyr Ser Gly Phe Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys
      180            185            190

Leu Ala Asn Thr Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala
      195            200            205

Val His Gly Tyr Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys
      210            215            220

Glu Thr Pro Glu Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu
      225            230            235            240

Leu Tyr Asp Leu Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr
      245            250            255

Asp Asp Leu Gly Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn
      260            265            270

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Ala Asn Lys Ala Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala  
 275 280 285

Asp Glu Thr Lys Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn  
 290 295 300

Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val  
 305 310 315 320

Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
 325 330

<210> 1073

<211> 437

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(414)

<223> FRXA01920

<400> 1073

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 Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr  
 1 5 10 15

tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag 96  
 Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu  
 20 25 30

cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt 144  
 Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu  
 35 40 45

tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga 192  
 Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly  
 50 55 60

tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc 240  
 Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala  
 65 70 75 80

ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag 288  
 Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys  
 85 90 95

gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac 336  
 Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn  
 100 105 110

cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca 384  
 His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala  
 115 120 125

gaa aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag 434  
 Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
 130 135

cgc

437

<210> 1074  
 <211> 138  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1074

Ala	Asp	Val	Ile	Arg	Leu	Ile	Ile	Arg	Asp	Glu	Ala	Val	His	Gly	Tyr
1				5					10					15	
Tyr	Ile	Gly	Tyr	Lys	Tyr	Gln	Lys	Ala	Val	Ala	Lys	Glu	Thr	Pro	Glu
		20						25					30		
Arg	Gln	Glu	Glu	Leu	Lys	Glu	Tyr	Thr	Phe	Asp	Leu	Leu	Tyr	Asp	Leu
		35					40					45			
Tyr	Asp	Asn	Glu	Thr	Gln	Tyr	Ser	Glu	Asp	Leu	Tyr	Asp	Asp	Leu	Gly
	50					55					60				
Trp	Thr	Glu	Asp	Val	Lys	Arg	Phe	Leu	Arg	Tyr	Asn	Ala	Asn	Lys	Ala
	65				70					75				80	
Leu	Asn	Asn	Leu	Gly	Tyr	Glu	Gly	Leu	Phe	Pro	Ala	Asp	Glu	Thr	Lys
			85					90						95	
Val	Ser	Pro	Asn	Ile	Leu	Ser	Ala	Leu	Ser	Pro	Asn	Ala	Asp	Glu	Asn
			100					105					110		
His	Asp	Phe	Phe	Ser	Gly	Ser	Gly	Ser	Ser	Tyr	Val	Ile	Gly	Lys	Ala
		115					120					125			
Glu	Asn	Thr	Glu	Asp	Asp	Asp	Trp	Asp	Phe						
	130					135									

<210> 1075  
 <211> 567  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA01080

<400> 1075

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ttgcgcacaa	acggtattta	gaagggaagt	gagttcgagg	atg cta atc gtg tat		115
				Met Leu Ile Val Tyr		
				1	5	
ttt tcc tgc gcc acc gac aac acg cat cgt ttt gta caa aag ctc gat						163
Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe Val Gln Lys Leu Asp						
	10		15		20	
tta ccc aac gtg cgc atc ccc ctc act agg gtg gaa gaa ccg ctg aaa						211
Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val Glu Glu Pro Leu Lys						
	25		30		35	



atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259  
 Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val  
 40 45 50  
 tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307  
 Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg  
 55 60 65  
 ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca 355  
 Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala  
 70 75 80 85  
 ggt gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc 403  
 Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile  
 90 95 100  
 att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg 451  
 Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met  
 105 110 115  
 ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac 499  
 Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn  
 120 125 130  
 gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga 544  
 Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg  
 135 140 145  
 taaaccttaa aacttaatca atc 567

&lt;210&gt; 1076

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1076

Met Leu Ile Val Tyr Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe  
 1 5 10 15  
 Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val  
 20 25 30  
 Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr  
 35 40 45  
 Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro  
 50 55 60  
 Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile  
 65 70 75 80  
 Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly  
 85 90 95  
 Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr  
 100 105 110  
 Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly  
 115 120 125

Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro  
 130 135 140

Val Thr Ser Arg  
 145

<210> 1077

<211> 650

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(627)

<223> RXA00867

<400> 1077

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Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr	
1 5 10 15	
gca ctt cag ctg gac acc aag ctg gac ggc att cct tcc aag gtg ctc	96
Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu	
20 25 30	
tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac	144
Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn	
35 40 45	
acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct	192
Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala	
50 55 60	
cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg	240
Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu	
65 70 75 80	
atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc	288
Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly	
85 90 95	
gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct	336
Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala	
100 105 110	
gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg	384
Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala	
115 120 125	
aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc	432
Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val	
130 135 140	
aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac	480
Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp	
145 150 155 160	
ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag	528
Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys	
165 170 175	

gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct 576  
 Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala  
                   180                                  185                                  190

gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag 624  
 Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu  
                   195                                  200                                  205

gac taattagttc tggctagatc ggg 650  
 Asp

<210> 1078

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 1078

Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr  
       1                                  5                                  10                                  15

Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu  
                                   20                                  25                                  30

Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn  
                   35                                  40                                  45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala  
                   50                                  55                                  60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu  
       65                                  70                                  75                                  80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly  
                                   85                                  90                                  95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala  
                   100                                  105                                  110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala  
                   115                                  120                                  125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val  
                   130                                  135                                  140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp  
       145                                  150                                  155                                  160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys  
                                   165                                  170                                  175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala  
                   180                                  185                                  190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu  
                   195                                  200                                  205

Asp

&lt;210&gt; 1079

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(630)

&lt;223&gt; RXA01416

&lt;400&gt; 1079

gct ggc gct tcc gaa aac gtt gtc aac cgc gtc aag gac ggt gca cca	48
Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro	
1 5 10 15	
gca cca acc gaa aag atc gtc tcc gac ggc ctt gaa gca gct aag cca	96
Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro	
20 25 30	
ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt	144
Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val	
35 40 45	
gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag	192
Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu	
50 55 60	
gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg	240
Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu	
65 70 75 80	
ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac	288
Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr	
85 90 95	
atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac	336
Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr	
100 105 110	
agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct	384
Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala	
115 120 125	
gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc	432
Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg	
130 135 140	
atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt	480
Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val	
145 150 155 160	
gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag	528
Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu	
165 170 175	
acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag	576
Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln	
180 185 190	

caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac 624  
 Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His  
           195                                  200                                  205

tac aac 630  
 Tyr Asn  
           210

<210> 1080

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1080

Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro  
           1                                  5                                  10                                  15

Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro  
                                   20                                  25                                  30

Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val  
                                   35                                  40                                  45

Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu  
           50                                  55                                  60

Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu  
           65                                  70                                  75                                  80

Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr  
                                   85                                  90                                  95

Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr  
                                   100                                  105                                  110

Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala  
           115                                  120                                  125

Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg  
           130                                  135                                  140

Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val  
           145                                  150                                  155                                  160

Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu  
                                   165                                  170                                  175

Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln  
                                   180                                  185                                  190

Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His  
           195                                  200                                  205

Tyr Asn  
           210

<210> 1081

<211> 757

<212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(757)

&lt;223&gt; RXA01486

&lt;400&gt; 1081

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agagaactgg taaggttttt accgttctag accgcagaaa tcttcgcggc gacaccgatg 60

atcgccgagc agaactaaac atgaggagac ctactcgcat atg agc gat gta aag 115
Met Ser Asp Val Lys
1 5

gac ttc gaa gac acc gaa ttt ggc ctg atc gag gcc gtc gca acc atc 163
Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu Ala Val Ala Thr Ile
10 15 20

gac aac ggt gac ttc gga acc cgc acc atc cgt ttt gaa acc ggc caa 211
Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg Phe Glu Thr Gly Gln
25 30 35

ctt gcc cgc cag gca gat ggt gca gtg acc acc tac ctc gac gat gac 259
Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr Tyr Leu Asp Asp Asp
40 45 50

acg atg ctg ctg gca acc acc acc gca tcc aac cag cca cgc gag ggc 307
Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn Gln Pro Arg Glu Gly
55 60 65

ttt gac ttc ttc cca ctg acc gtg gac gtt gaa gag cgt atg tac gca 355
Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu Glu Arg Met Tyr Ala
70 75 80 85

gct ggt cgc atc cct ggc tct ttc ttc cgt cgg gag ggt cgc cca tcc 403
Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg Glu Gly Arg Pro Ser
90 95 100

acc gaa gct atc ctg gct tgc cgt ctc atc gac cgc cca ctg cgc cca 451
Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp Arg Pro Leu Arg Pro
105 110 115

acc ttt gtt aag ggc ctg cgc aat gag gtt cag atc gtt gtc acc gtc 499
Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln Ile Val Val Thr Val
120 125 130

atg tcc atg aac cct gag gat tac tac gat gtc gta gca atc aac gga 547
Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val Val Ala Ile Asn Gly
135 140 145

gct tcc gca gca acc cgc atc tcc gga ctt cct gtc tcc ggc gct gtc 595
Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro Val Ser Gly Ala Val
150 155 160 165

ggt ggc gtt cgc atg gca ctg gtt ggt gat gaa aag cac cca gaa ggc 643
Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu Lys His Pro Glu Gly
170 175 180

caa tgg gtt gca ttc cca acc cac gct caa cat gag cag tcc gta ttt 691
Gln Trp Val Ala Phe Pro Thr His Ala Gln His Glu Gln Ser Val Phe
185 190 195

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gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739  
 Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg Lys Arg Gly Asn Lys  
           200                          205                          210

acc ttc tcc gac gtc gca 757  
 Thr Phe Ser Asp Val Ala  
           215

<210> 1082

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1082

Met Ser Asp Val Lys Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu  
       1                          5                          10                          15

Ala Val Ala Thr Ile Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg  
                           20                          25                          30

Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr  
                           35                          40                          45

Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn  
           50                          55                          60

Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu  
       65                          70                          75                          80

Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg  
                           85                          90                          95

Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp  
                           100                          105                          110

Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln  
           115                          120                          125

Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val  
       130                          135                          140

Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro  
       145                          150                          155                          160

Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu  
                           165                          170                          175

Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His  
                           180                          185                          190

Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg  
           195                          200                          205

Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala  
       210                          215

<210> 1083

<211> 651

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(628)

&lt;223&gt; RXA01678

&lt;400&gt; 1083

tattgtccag gcgcaggaaa atatctcata gttcaacatc gcaaatatca ccgacttcca 60

eggctatatc	tctgcaactg	cagctcaccc	cggtgcagca	atg	ctg	aaa	tgt	gca	115
				Met	Leu	Lys	Cys	Ala	
				1				5	

gtc	gat	gaa	gcc	gct	ggc	gga	cgc	gcc	caa	gct	ttc	gta	tcc	tca	ggc	163
Val	Asp	Glu	Ala	Ala	Gly	Gly	Arg	Ala	Gln	Ala	Phe	Val	Ser	Ser	Gly	
			10					15					20			

gat	aac	att	ggt	ggc	agc	ccg	ttc	caa	tcc	tcc	att	ctt	ggt	gat	gaa	211
Asp	Asn	Ile	Gly	Gly	Ser	Pro	Phe	Gln	Ser	Ser	Ile	Leu	Gly	Asp	Glu	
			25				30						35			

ccc	acc	ttg	gaa	gca	ctc	aac	caa	atg	ggt	ctt	gat	tac	tca	gca	gtg	259
Pro	Thr	Leu	Glu	Ala	Leu	Asn	Gln	Met	Gly	Leu	Asp	Tyr	Ser	Ala	Val	
		40				45						50				

ggc	aac	cac	gaa	ttt	gat	aaa	ggc	tac	gca	gac	tta	agc	agt	cga	gtc	307
Gly	Asn	His	Glu	Phe	Asp	Lys	Gly	Tyr	Ala	Asp	Leu	Ser	Ser	Arg	Val	
	55					60					65					

gct	gac	ctt	gct	gat	ttt	gat	tat	ctc	ggc	gca	aac	gtt	gag	ggc	gaa	355
Ala	Asp	Leu	Ala	Asp	Phe	Asp	Tyr	Leu	Gly	Ala	Asn	Val	Glu	Gly	Glu	
70					75				80					85		

aac	cca	gat	ctt	gca	cca	tat	gga	att	tct	cac	ctt	gat	ggt	gtg	aag	403
Asn	Pro	Asp	Leu	Ala	Pro	Tyr	Gly	Ile	Ser	His	Leu	Asp	Gly	Val	Lys	
			90					95					100			

gtt	gct	ttc	gta	ggc	acc	gta	tcc	caa	gaa	act	ccg	atg	ttg	gtc	aat	451
Val	Ala	Phe	Val	Gly	Thr	Val	Ser	Gln	Glu	Thr	Pro	Met	Leu	Val	Asn	
			105					110					115			

tct	gaa	ggc	att	gag	gga	atc	acg	ttt	act	gac	cca	ctt	gaa	gca	acc	499
Ser	Glu	Gly	Ile	Glu	Gly	Ile	Thr	Phe	Thr	Asp	Pro	Leu	Glu	Ala	Thr	
		120				125						130				

aac	cgt	gta	gct	gat	gaa	ctc	gtg	gga	agt	ggc	gca	gca	gat	gtt	gtc	547
Asn	Arg	Val	Ala	Asp	Glu	Leu	Val	Gly	Ser	Gly	Ala	Ala	Asp	Val	Val	
	135					140					145					

gtt	gcg	ctt	tac	cac	gaa	ggc	att	acc	ggc	acc	gaa	gca	tgg	tca	gaa	595
Val	Ala	Leu	Tyr	His	Glu	Gly	Ile	Thr	Gly	Thr	Glu	Ala	Trp	Ser	Glu	
150					155				160					165		

aat	atc	gac	gtt	gtt	ttc	gca	ggt	cac	acc	cac	taagttcgtg	atctaggaac	648
Asn	Ile	Asp	Val	Val	Phe	Ala	Gly	His	Thr	His			
			170					175					

cga

651



&lt;210&gt; 1084

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1084

Met Leu Lys Cys Ala Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala  
 1 5 10 15

Phe Val Ser Ser Gly Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser  
 20 25 30

Ile Leu Gly Asp Glu Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu  
 35 40 45

Asp Tyr Ser Ala Val Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp  
 50 55 60

Leu Ser Ser Arg Val Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala  
 65 70 75 80

Asn Val Glu Gly Glu Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His  
 85 90 95

Leu Asp Gly Val Lys Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr  
 100 105 110

Pro Met Leu Val Asn Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp  
 115 120 125

Pro Leu Glu Ala Thr Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly  
 130 135 140

Ala Ala Asp Val Val Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr  
 145 150 155 160

Glu Ala Trp Ser Glu Asn Ile Asp Val Val Phe Ala Gly His Thr His  
 165 170 175

&lt;210&gt; 1085

&lt;211&gt; 1359

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1336)

&lt;223&gt; RXA01679

&lt;400&gt; 1085

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ctaagttcgt gatctaggaa ccgacaacgg tccactaatc atg cag tct gga aac 115  
 Met Gln Ser Gly Asn  
 1 5

tac ggg cac gca ctt gcc gat gta gat ttc agc ttc aac cac gac acc	163
Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr	
10 15 20	
ggt gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc	211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Asp Ile	
25 30 35	
aac gcg tgt gaa aac cca gat gac acc att gca gat att gtt gct cag	259
Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala Asp Ile Val Ala Gln	
40 45 50	
gcg gaa ctt gat gct ggt gaa gcc ggc aaa gaa gta gta gcg acc atc	307
Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu Val Val Ala Thr Ile	
55 60 65	
gat ggc gat ttt ctc cgc gcc agc gac gaa gga gca gaa tct ggc tcc	355
Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly Ala Glu Ser Gly Ser	
70 75 80 85	
aac tac ggc gct gaa tcc cag ctc gtc aac atg att gcc agt gct gtg	403
Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met Ile Ala Ser Ala Val	
90 95 100	
cgt tgg tcc atg tcc acc aat acc gcc acc acc gca gac att ggg ctt	451
Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr Ala Asp Ile Gly Leu	
105 110 115	
atg aac gcc gga gga ctc cac act gac cta ttc agc ggc gat gtt acc	499
Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe Ser Gly Asp Val Thr	
120 125 130	
tac gcc gaa gct ttt gaa atc cag cct ttc tcc ggt gaa gat tca ttt	547
Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser Gly Glu Asp Ser Phe	
135 140 145	
gtc acc ctc aag gga tca gtc ttc aaa gat gcc ctt gac cag cag tgg	595
Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala Leu Asp Gln Gln Trp	
150 155 160 165	
gaa gaa ggt tct gca cga cca gtg gca gca ctt ggc gta tcc gac aac	643
Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu Gly Val Ser Asp Asn	
170 175 180	
gtt tcc tac acc tac gac atc aac cgt cca atc ggt gac cgc gtc act	691
Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile Gly Asp Arg Val Thr	
185 190 195	
tcc gtg acc att gat gat acc cca ctt gat ccg gaa cgc gac tac gtt	739
Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro Glu Arg Asp Tyr Val	
200 205 210	
gtt gca gct tcc ctg tac ctc cag tcc ggc aac gaa ggt atg acc gca	787
Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn Glu Gly Met Thr Ala	
215 220 225	
ctg acc cgc gga acc gca cct gca caa acc ggc atc gtg gat gta cag	835
Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly Ile Val Asp Val Gln	
230 235 240 245	
tcc acc atc gga tac ttg tcc aac aac aat gtc acc cca cgt act ggt	883

Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val Thr Pro Arg Thr Gly  
 250 255 260  
 caa gcc cag att tcc atc acc cca tcc ggt gag ttc aat gcg ggt gaa 931  
 Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu Phe Asn Ala Gly Glu  
 265 270 275  
 acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979  
 Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr  
 280 285 290  
 gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca  
 1027  
 Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro  
 295 300 305  
 att gat cct cag ctc gga gaa gct ggc ttt ggc gaa gct gga acc gcg  
 1075  
 Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala  
 310 315 320 325  
 aca gtg agc ttg gac att cct gca acc ctt tca ggt act caa aac ctc  
 1123  
 Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser Gly Thr Gln Asn Leu  
 330 335 340  
 gtt gtc acc acc gat acc ggc acc cgt att tcc atg cca gtt gag att  
 1171  
 Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser Met Pro Val Glu Ile  
 345 350 355  
 gtt ggc gca gaa caa cca gca ccg caa cca gca ggt tcc tct gtt tta  
 1219  
 Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala Gly Ser Ser Val Leu  
 360 365 370  
 gga act gga gtg ctc agt gga ctc ctc ggc att gtt gta gga att cta  
 1267  
 Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile Val Val Gly Ile Leu  
 375 380 385  
 gga atg gtc ggt ctg gtg aac tgg att gac cca agc ttc att caa cag  
 1315  
 Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln  
 390 395 400 405  
 atc cag cag caa atc ttt gct taaatttagt aaaaagcatg cat  
 1359  
 Ile Gln Gln Gln Ile Phe Ala  
 410

&lt;210&gt; 1086

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1086

Met Gln Ser Gly Asn Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser  
 1 5 10 15

Phe Asn His Asp Thr Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu  
 20 25 30  
 Gly Val Asp Asp Ile Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala  
 35 40 45  
 Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu  
 50 55 60  
 Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly  
 65 70 75 80  
 Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met  
 85 90 95  
 Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr  
 100 105 110  
 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe  
 115 120 125  
 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser  
 130 135 140  
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala  
 145 150 155 160  
 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu  
 165 170 175  
 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile  
 180 185 190  
 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro  
 195 200 205  
 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn  
 210 215 220  
 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly  
 225 230 235 240  
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val  
 245 250 255  
 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu  
 260 265 270  
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr  
 275 280 285  
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu  
 290 295 300  
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly  
 305 310 315 320  
 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser  
 325 330 335  
 Gly Thr Gln Asn Leu Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser

340	345	350
Met Pro Val Glu Ile Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala		
355	360	365
Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile		
370	375	380
Val Val Gly Ile Leu Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro		
385	390	395
400		
Ser Phe Ile Gln Gln Ile Gln Gln Gln Ile Phe Ala		
405	410	

&lt;210&gt; 1087

&lt;211&gt; 1071

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1048)

&lt;223&gt; RXN01488

&lt;400&gt; 1087

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gcccgcacctt aaaaataaaa acctgaaagg ttaaaaacgc atg agc aaa aaa gcc 115
                                         Met Ser Lys Lys Ala
                                         1           5
atc ctt gat atc gac acc ggc atc gat gat gcc ctc gca ctt gcc tac 163
Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ala Tyr
                        10           15           20
gca ctg ggc tca cct gaa cta gag ctc att ggt gtc acc acc acc tac 211
Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly Val Thr Thr Thr Tyr
                        25           30           35
ggt aac gtg cta ctc gaa acc ggt gca gtc aat gac ctg gca ctg ctt 259
Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu
                        40           45           50
gat ctg ttc ggt gca cca gaa gta cct gtg tac ttg ggt gag cca cac 307
Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His
                        55           60           65
gca cag acc aag gat ggc ttt gaa gtt ctt gag atc tcc gcg ttc att 355
Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile
                        70           75           80           85
cac gga caa aac ggc atc ggc gaa gtc gag ctg cca gca agc gag tca 403
His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser
                        90           95           100
aag gca ctc ccc ggc gca gtg gat ttc ctc att gat tcc gtc aac acc 451
Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr
                        105           110           115
cac ggc gat gac ctg gtg atc atc gca act ggt ccc atg acc aac ctg 499

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His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu  
 120 125 130

tct gcg gca atc gca aag gat cca agc ttt gct tcc aag gct cac gtg 547  
 Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val  
 135 140 145

gtc atc atg ggt ggc gcc ttg act gtc cca ggc aac gtc agc aca tgg 595  
 Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp  
 150 155 160 165

gca gaa gca aac atc aac cag gac cca gat gca gca aac gat ctg ttc 643  
 Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe  
 170 175 180

cgt tcc ggt gca gat gtc acc atg atc ggt ctt gat gtc acc ctg cag 691  
 Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln  
 185 190 195

acc ctt ctt acc aag aag cac act gcg cag tgg cgc gaa ctg ggc act 739  
 Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr  
 200 205 210

cca gct gct atc gca ctg gcc gac atg act gat tac tac atc aag gca 787  
 Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala  
 215 220 225

tat gag acc acc gca cca cac ctg ggc ggt tgc ggc ctg cac gac cca 835  
 Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro  
 230 235 240 245

ctg gca gta ggc gtt gca gtg gac cca agc ctg gtc act ttg ctc ccc 883  
 Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro  
 250 255 260

atc aac ctc aag gta gac att gag ggc gag acc cgt gga cgc acc att 931  
 Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile  
 265 270 275

ggc gat gaa gtc cgc ctc aac gat cca gtg cgc acc tcc cgc gca gct 979  
 Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala  
 280 285 290

gtc gcc gta gac gtg gat cgt ttc ctt tct gaa ttc atg acc cgc atc  
 1027  
 Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile  
 295 300 305

ggc cga gtc gca gca cag cag taaaagcagc tctggtgaag gtt  
 1071  
 Gly Arg Val Ala Ala Gln Gln  
 310 315

<210> 1088  
 <211> 316  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1088  
 Met Ser Lys Lys Ala Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala

1	5	10	15
Leu Ala Leu Ala Tyr Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly	20	25	30
Val Thr Thr Thr Tyr Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn	35	40	45
Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr	50	55	60
Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu	65	70	75
Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu	85	90	95
Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile	100	105	110
Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly	115	120	125
Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala	130	135	140
Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly	145	150	155
Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala	165	170	175
Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu	180	185	190
Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp	195	200	205
Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp	210	215	220
Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys	225	230	235
Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu	245	250	255
Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr	260	265	270
Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg	275	280	285
Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu	290	295	300
Phe Met Thr Arg Ile Gly Arg Val Ala Ala Gln Gln	305	310	315

&lt;210&gt; 1089





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<210> 1091
<211> 498
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(475)  
<223> RXC00560
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<400> 1091																		
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catatggaca				ctttaacggt	tcgtactagg	ctgatgcttc	atg	agg	att	gat	ccg						115	
							Met	Arg	Ile	Asp	Pro							
							1						5					
ctg	gaa	acc	cgg	caa	gcc	gta	ttg	gcc	gtc	aaa	gac	tgg	att	gaa	ggg	163		
Leu	Glu	Thr	Arg	Gln	Ala	Val	Leu	Ala	Val	Lys	Asp	Trp	Ile	Glu	Gly			
				10					15					20				
gag	gga	gac	gtc	aaa	aag	cct	ggt	cgt	gcg	gca	ctt	gcc	gcc	gca	act	211		
Glu	Gly	Asp	Val	Lys	Lys	Pro	Gly	Arg	Ala	Ala	Leu	Ala	Ala	Ala	Thr			
				25					30					35				
cgc	ctg	agc	gtc	cga	ctg	ctc	gcg	caa	cac	gcg	ccg	gga	aac	agc	gtg	259		
Arg	Leu	Ser	Val	Arg	Leu	Leu	Ala	Gln	His	Ala	Pro	Gly	Asn	Ser	Val			
				40					45					50				
gag	gtg	cgg	gta	ccc	cca	ttt	gtt	gcg	gtg	caa	tgc	ata	gag	ggg	cca	307		
Glu	Val	Arg	Val	Pro	Pro	Phe	Val	Ala	Val	Gln	Cys	Ile	Glu	Gly	Pro			
				55					60					65				
aaa	cat	aca	cgc	ggc	aca	cca	ccc	aac	gtg	gtg	gag	acc	gac	gcc	aag	355		
Lys	His	Thr	Arg	Gly	Thr	Pro	Pro	Asn	Val	Val	Glu	Thr	Asp	Ala	Lys			
				70					75					80			85	
acc	tgg	tta	cgc	tta	gca	cct	ggg	caa	acc	aca	ttt	gat	gca	gaa	ttt	403		
Thr	Trp	Leu	Arg	Leu	Ala	Pro	Gly	Gln	Thr	Thr	Phe	Asp	Ala	Glu	Phe			
				90					95					100				
gaa	agc	gga	aaa	att	agc	gca	tca	ggt	acc	cga	gcc	aaa	gag	att	gcg	451		
Glu	Ser	Gly	Lys	Ile	Ser	Ala	Ser	Gly	Thr	Arg	Ala	Lys	Glu	Ile	Ala			
				105					110					115				
gac	tgg	tta	cca	gtg	gtc	aaa	ctt	tagatttcct				aatgctcatt				agt	498	
Asp	Trp	Leu	Pro	Val	Val	Lys	Leu											
				120					125									

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<210> 1092
<211> 125
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1092
Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys
  1             5             10             15
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Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala  
                   20                                  25                                  30  
 Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala  
                   35                                  40                                  45  
 Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln  
                   50                                  55                                  60  
 Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val  
                   65                                  70                                  75                                  80  
 Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr  
                                   85                                  90                                  95  
 Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg  
                   100                                  105                                  110  
 Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu  
                   115                                  120                                  125

&lt;210&gt; 1093

&lt;211&gt; 1305

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1282)

&lt;223&gt; RXC01088

&lt;400&gt; 1093

tgccttgagt ctaattctcc cgcccgtagc atgggtttaa gctggactga taaacctttt 60

gtgaaccgaa ttttttaact gatttgaaga agcgagaata atg gga ctg tgg atc 115  
   Met Gly Leu Trp Ile  
   1                                  5

gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163  
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile  
                                   10                                  15                                  20

gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211  
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val  
                                   25                                  30                                  35

atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259  
 Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly  
                   40                                  45                                  50

caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat 307  
 Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His  
                   55                                  60                                  65

cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc 355  
 His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile  
                   70                                  75                                  80                                  85

cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct 403

Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala  
90 95 100

atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc 451  
Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe  
105 110 115

cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc 499  
His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys  
120 125 130

gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att 547  
Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile  
135 140 145

gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg 595  
Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His Gly Asp Ile Pro Val  
150 155 160 165

cca gtt cca gcc gtg gca gag ctg gtg aaa ggc tgg ccc acc caa acc 643  
Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly Trp Pro Thr Gln Thr  
170 175 180

gga gct ctt atg gag agc acc gaa cct gtt ggt gaa tta gcc acc cca 691  
Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly Glu Leu Ala Thr Pro  
185 190 195

act ggt gtt gcg ttg atc cgt cac ttt gcc acc caa gat ggc cct ttc 739  
Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr Gln Asp Gly Pro Phe  
200 205 210

cca ggt ggc atc atc aat gaa gtt ggc att ggt gca gga aca aaa gat 787  
Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly Ala Gly Thr Lys Asp  
215 220 225

aca gaa ggc cgt cca aat ata gtg cgc gca att ttg ttc aac acc tct 835  
Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile Leu Phe Asn Thr Ser  
230 235 240 245

agg agt aac cca gat acc cgc aca ctg gtg caa tta gaa gcc aat gtt 883  
Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln Leu Glu Ala Asn Val  
250 255 260

gat gat caa gac cca cgg ctg tgg cca gga gta ata gag atc ctc ttt 931  
Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val Ile Glu Ile Leu Phe  
265 270 275

gcc gct ggc gca gta gat gca tgg ctg act cca att ttg atg aag aag 979  
Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro Ile Leu Met Lys Lys  
280 285 290

ggc cgt cct gca cat agg gtg tca gca ttg gtg gat agc tcc gag gtg  
1027  
Gly Arg Pro Ala His Arg Val Ser Ala Leu Val Asp Ser Ser Glu Val  
295 300 305

gaa gca gtg aaa acc gca tta ttt gca gcc acc acg act ttt ggg atc  
1075  
Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr Thr Thr Phe Gly Ile  
310 315 320 325

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa  
1123

Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln  
330 335 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat  
1171

Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp  
345 350 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca  
1219

Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala  
360 365 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg  
1267

Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro  
375 380 385

caa ggc acc acc gag taacaaccaa aaggtcgact gct  
1305

Gln Gly Thr Thr Glu  
390

<210> 1094

<211> 394

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1094

Met Gly Leu Trp Ile Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu  
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Leu Gly Ala Leu Ile Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln  
20 25 30

Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu  
35 40 45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln  
50 55 60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu  
65 70 75 80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val  
85 90 95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro  
100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp  
115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile  
130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His  
145 150 155 160

Gly	Asp	Ile	Pro	Val	Pro	Ala	Val	Ala	Glu	Leu	Val	Lys	Gly
				165				170				175	
Trp	Pro	Thr	Gln	Thr	Gly	Ala	Leu	Met	Glu	Ser	Thr	Glu	Pro
			180					185				190	Val Gly
Glu	Leu	Ala	Thr	Pro	Thr	Gly	Val	Ala	Leu	Ile	Arg	His	Phe
		195					200				205	Ala Thr	
Gln	Asp	Gly	Pro	Phe	Pro	Gly	Gly	Ile	Ile	Asn	Glu	Val	Gly
	210					215					220	Ile Gly	
Ala	Gly	Thr	Lys	Asp	Thr	Glu	Gly	Arg	Pro	Asn	Ile	Val	Arg
225					230					235		Ala Ile	
Leu	Phe	Asn	Thr	Ser	Arg	Ser	Asn	Pro	Asp	Thr	Arg	Thr	Leu
				245					250			Val Gln	
Leu	Glu	Ala	Asn	Val	Asp	Asp	Gln	Asp	Pro	Arg	Leu	Trp	Pro
			260					265				Gly Val	
Ile	Glu	Ile	Leu	Phe	Ala	Ala	Gly	Ala	Val	Asp	Ala	Trp	Leu
		275					280					285	Thr Pro
Ile	Leu	Met	Lys	Lys	Gly	Arg	Pro	Ala	His	Arg	Val	Ser	Ala
	290					295					300	Leu Val	
Asp	Ser	Ser	Glu	Val	Glu	Ala	Val	Lys	Thr	Ala	Leu	Phe	Ala
305					310					315		Ala Thr	
Thr	Thr	Phe	Gly	Ile	Arg	Ser	Trp	Glu	Val	Glu	Arg	Glu	Gly
			325						330			Leu Asp	
Arg	Arg	Phe	Glu	Gln	Val	Glu	Val	Asp	Gly	His	Thr	Ile	Asn
			340					345				350	Ile Lys
Ile	Gly	Ser	Arg	Asp	Asp	Gln	Val	Ile	Ser	Ala	Gln	Ser	Glu
		355					360					365	Phe Glu
Asp	Ile	Arg	Ser	Ala	Ala	Val	Ala	Leu	Gly	Ile	Ser	Glu	Arg
	370					375					380	Glu Val	
Val	Ala	Arg	Ile	Pro	Gln	Gly	Thr	Thr	Glu				
385					390								

<210> 1095

<211> 1419

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1396)

<223> RXC02624

<400> 1095

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ggcagctcag caatcaaagt tgctgcgttt ccttccaacc gtg ctg att ccg cat 115

												Val	Leu	Ile	Pro	His	
												1				5	
ggc	gtg	gcg	gtg	ctt	ttg	gtt	att	att	ctc	gcc	gta	gcc	tcc	cta	atg		163
Gly	Val	Ala	Val	Leu	Leu	Val	Ile	Ile	Leu	Ala	Val	Ala	Ser	Leu	Met		
				10					15					20			
ttc	acc	aat	tct	tca	atg	gtg	aat	ctt	tgc	gca	acg	att	gca	cag	ctg		211
Phe	Thr	Asn	Ser	Ser	Met	Val	Asn	Leu	Ser	Ala	Thr	Ile	Ala	Gln	Leu		
			25					30					35				
tgg	ctt	tcc	cta	aat	ctc	ggt	gcg	gtg	gac	ggc	agt	ggg	gaa	gtg	atc		259
Trp	Leu	Ser	Leu	Asn	Leu	Gly	Ala	Val	Asp	Gly	Ser	Gly	Glu	Val	Ile		
		40					45					50					
tca	gta	ctg	ccc	acg	ctt	ccc	ggc	ttt	ata	ttc	ctc	tgg	gcc	atc	gcc		307
Ser	Val	Leu	Pro	Thr	Leu	Pro	Gly	Phe	Ile	Phe	Leu	Trp	Ala	Ile	Ala		
	55					60					65						
gcg	cgc	atc	cac	cgc	gca	gtc	aaa	gat	cgt	gtc	agc	atc	gcc	gac	tta		355
Ala	Arg	Ile	His	Arg	Ala	Val	Lys	Asp	Arg	Val	Ser	Ile	Ala	Asp	Leu		
70				75					80						85		
ggc	gtc	ctc	gca	gca	ctc	gtc	ctc	ggc	atc	ccg	ctt	gcg	ctc	acc	gcc		403
Gly	Val	Leu	Ala	Ala	Leu	Val	Leu	Gly	Ile	Pro	Leu	Ala	Leu	Thr	Ala		
			90					95						100			
atc	gca	gcg	ttc	atg	ctt	ttc	gac	gcc	tcc	agc	gtc	ctc	aac	gtc	gag		451
Ile	Ala	Ala	Phe	Met	Leu	Phe	Asp	Ala	Ser	Ser	Val	Leu	Asn	Val	Glu		
			105					110					115				
gtc	ccg	cca	atc	acg	cgc	ctc	cta	cgc	gtg	atg	ttg	ttc	cac	ctc	agc		499
Val	Pro	Pro	Ile	Thr	Arg	Leu	Leu	Arg	Val	Met	Leu	Phe	His	Leu	Ser		
		120					125					130					
gcc	ctc	ttc	ctc	ggc	atg	ggg	cca	cgc	ctg	tgg	cag	gcg	ttg	gcg	cgc		547
Ala	Leu	Phe	Leu	Gly	Met	Gly	Pro	Arg	Leu	Trp	Gln	Ala	Leu	Ala	Arg		
	135					140					145						
cgc	tac	ggt	gct	cca	gaa	tgg	ctt	atc	gac	gcc	atc	acc	caa	gct	ttc		595
Arg	Tyr	Gly	Ala	Pro	Glu	Trp	Leu	Ile	Asp	Ala	Ile	Thr	Gln	Ala	Phe		
150					155				160						165		
cgc	ttc	ctc	atc	gca	ttt	gga	aca	gtc	tcc	ttg	gtt	tcc	gtg	ctc	gtg		643
Arg	Phe	Leu	Ile	Ala	Phe	Gly	Thr	Val	Ser	Leu	Val	Ser	Val	Leu	Val		
				170				175						180			
atg	acc	gcg	atc	aac	cac	agt	gca	ttc	acc	gcg	acc	atg	cag	ggt	tac		691
Met	Thr	Ala	Ile	Asn	His	Ser	Ala	Phe	Thr	Ala	Thr	Met	Gln	Gly	Tyr		
			185					190					195				
gac	gac	tcc	gcc	tct	gtt	gtg	gcc	ttg	atc	gtc	ctg	agc	att	ctg	tat		739
Asp	Asp	Ser	Ala	Ser	Val	Val	Ala	Leu	Ile	Val	Leu	Ser	Ile	Leu	Tyr		
		200					205					210					
ctg	ccc	aac	atg	atg	atc	ttt	gcg	atg	ggc	aat	ctg	atc	ggc	tca	ccc		787
Leu	Pro	Asn	Met	Met	Ile	Phe	Ala	Met	Gly	Asn	Leu	Ile	Gly	Ser	Pro		
	215					220					225						
ctt	tac	ttc	ggt	gac	gcc	tcc	atc	agc	gtc	ttc	agc	gtg	cat	tcc	gtt		835
Leu	Tyr	Phe	Gly	Asp	Ala	Ser	Ile	Ser	Val	Phe	Ser	Val	His	Ser	Val		

230	235	240	245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc				883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu	250	255	260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg				931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp	265	270	275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca				979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala	280	285	290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga				
1027				
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly	295	300	305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt				
1075				
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val	310	315	320	325
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga				
1123				
Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly	330	335	340	
atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg				
1171				
Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val	345	350	355	
gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag				
1219				
Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu	360	365	370	
cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg				
1267				
His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly	375	380	385	
gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct				
1315				
Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro	390	395	400	405
gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa				
1363				
Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu	410	415	420	
gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt				
1416				
Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg	425	430		

ctg  
1419

&lt;210&gt; 1096

&lt;211&gt; 432

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1096

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala  
 1 5 10 15

Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala  
 20 25 30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly  
 35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe  
 50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val  
 65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro  
 85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser  
 100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met  
 115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp  
 130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala  
 145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu  
 165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala  
 180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val  
 195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn  
 210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe  
 225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu  
 245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala  
 260 265 270

Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val  
 275 280 285



Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala  
 290 295 300  
 Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn  
 305 310 315 320  
 Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly  
 325 330 335  
 Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys  
 340 345 350  
 Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu  
 355 360 365  
 Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu  
 370 375 380  
 Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp  
 385 390 395 400  
 Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr  
 405 410 415  
 Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg  
 420 425 430

&lt;210&gt; 1097

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; RXC02665

&lt;400&gt; 1097

caaggcgacc caatggcggtt taaagtaaca acccccattg atatgatgct ggcacaacgc 60  
 atcaccgacg aagccgaacc cacaatattt gaggtaccag gtg act aac cca atc 115  
 Val Thr Asn Pro Ile  
 1 5  
 atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga 163  
 Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly  
 10 15 20  
 aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211  
 Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys  
 25 30 35  
 gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259  
 Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala  
 40 45 50

ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg 307  
 Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val  
     55                    60                    65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355  
 Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu  
     70                    75                    80                    85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403  
 Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala  
                     90                    95                    100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa 451  
 Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu  
                     105                    110                    115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct 499  
 Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser  
                     120                    125                    130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547  
 Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg  
                     135                    140                    145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600  
 Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala  
     150                    155                    160

ggc 603

<210> 1098

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 1098

Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His  
     1                    5                    10                    15

Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu  
                     20                    25                    30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His  
                     35                    40                    45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly  
                     50                    55                    60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr  
     65                    70                    75                    80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val  
                     85                    90                    95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly  
                     100                    105                    110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala  
                     115                    120                    125

Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly  
 130 135 140

Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala  
 145 150 155 160

<210> 1099  
 <211> 1689  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1666)  
 <223> RXC02770

<400> 1099  
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ttcacacatg ttgtttcggga agtcacgcag cgccggtaatc atg ttg gtt gca gcg 115  
 Met Leu Val Ala Ala  
 1 5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163  
 Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His  
 10 15 20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcc ctg gct aca acc 211  
 Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr  
 25 30 35

aac gcg gcg tcc ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259  
 Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala  
 40 45 50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307  
 Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met  
 55 60 65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355  
 Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn  
 70 75 80 85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403  
 Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly  
 90 95 100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451  
 Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln  
 105 110 115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcc cag att gag 499  
 Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu  
 120 125 130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547  
 Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys

135	140	145	
gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu 150 155 160 165			595
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu 170 175 180			643
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro 185 190 195			691
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu 200 205 210			739
ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg ggt gaa ttc Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe 215 220 225			787
ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala 230 235 240 245			835
gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala 250 255 260			883
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu 265 270 275			931
agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile 280 285 290			979
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc 1027 Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala 295 300 305			
ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt 1075 Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val 310 315 320 325			
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat 1123 Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp 330 335 340			
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg 1171 Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val 345 350 355			
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat 1219 His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn			

360                      365                      370  
 gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga  
 1267  
 Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly  
 375                      380                      385  
  
 ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt  
 1315  
 Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys  
 390                      395                      400                      405  
  
 gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt  
 1363  
 Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser  
 410                      415                      420  
  
 ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag  
 1411  
 Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln  
 425                      430                      435  
  
 tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat  
 1459  
 Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His  
 440                      445                      450  
  
 cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg  
 1507  
 Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr  
 455                      460                      465  
  
 agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta  
 1555  
 Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu  
 470                      475                      480                      485  
  
 gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt  
 1603  
 Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val  
 490                      495                      500  
  
 gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg  
 1651  
 Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp  
 505                      510                      515  
  
 tcc aga agt gag gaa taagtagtga gcgaacaagc tct  
 1689  
 Ser Arg Ser Glu Glu  
 520

&lt;210&gt; 1100

&lt;211&gt; 522

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1100

Met Leu Val Ala Ala Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro

1

5

10

15

Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser  
 20 25 30  
 Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp  
 35 40 45  
 Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly  
 50 55 60  
 Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val  
 65 70 75 80  
 Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala  
 85 90 95  
 Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser  
 100 105 110  
 Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu  
 115 120 125  
 Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala  
 130 135 140  
 Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe  
 145 150 155 160  
 Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly  
 165 170 175  
 Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu  
 180 185 190  
 Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser  
 195 200 205  
 Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp  
 210 215 220  
 Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr  
 225 230 235 240  
 Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly  
 245 250 255  
 Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His  
 260 265 270  
 Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu  
 275 280 285  
 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu  
 290 295 300  
 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala  
 305 310 315 320  
 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser  
 325 330 335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His  
 340 345 350

Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met  
 355 360 365

Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg  
 370 375 380

Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala  
 385 390 395 400

Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser  
 405 410 415

Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu  
 420 425 430

Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg  
 435 440 445

Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr  
 450 455 460

Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val  
 465 470 475 480

Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg  
 485 490 495

Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp  
 500 505 510

Asn Met Asp Arg Trp Ser Arg Ser Glu Glu  
 515 520

&lt;210&gt; 1101

&lt;211&gt; 408

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; RXC02238

&lt;400&gt; 1101

ggcgcttagc caaaacatag agcggtaggg tatgcttatc cgattgagca acctttcccg 60

ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115  
 Val Thr Asn Val Ser  
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr  
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
           40                          45                          50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
           55                          60                          65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
           70                          75                          80                          85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                           90                          95

cac 408

<210> 1102

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1102

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp  
           1                          5                          10                          15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys  
                           20                          25                          30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg  
           35                          40                          45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe  
           50                          55                          60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile  
           65                          70                          75                          80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                           85                          90                          95

<210> 1103

<211> 1298

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1275)

<223> RXC01946

<400> 1103

atc cgc aag tac tcc agg ctc gag gaa caa ttc cag tcg ctc ggc ggc 48  
 Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly  
           1                          5                          10                          15

tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96



Tyr	Glu	Ala	Asp	Ala	Glu	Ala	Ala	Gln	Ile	Cys	Asp	Asn	Leu	Gly	Leu	
			20					25					30			
gag	gca	cgc	atc	ctc	gac	cag	cag	ctt	aaa	acc	ctg	tcc	ggc	ggc	cag	144
Glu	Ala	Arg	Ile	Leu	Asp	Gln	Gln	Leu	Lys	Thr	Leu	Ser	Gly	Gly	Gln	
		35				40					45					
cgc	cgc	cgc	gtc	gag	ttg	gcg	cag	atc	ctc	ttc	gcc	gcc	acc	aac	ggc	192
Arg	Arg	Arg	Val	Glu	Leu	Ala	Gln	Ile	Leu	Phe	Ala	Ala	Thr	Asn	Gly	
	50					55				60						
tcc	ggc	aaa	tca	aaa	acc	aca	ttg	ctt	ctc	gac	gag	ccc	acc	aac	cac	240
Ser	Gly	Lys	Ser	Lys	Thr	Thr	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His	
65					70				75					80		
ttg	gac	gca	gac	tcg	atc	acc	tgg	ctc	cgt	gac	ttc	ctg	gcg	aag	cac	288
Leu	Asp	Ala	Asp	Ser	Ile	Thr	Trp	Leu	Arg	Asp	Phe	Leu	Ala	Lys	His	
				85				90						95		
gaa	ggt	gga	ctg	atc	atg	att	tcg	cac	gac	gtc	gaa	ctg	ctt	ggc	gcc	336
Glu	Gly	Gly	Leu	Ile	Met	Ile	Ser	His	Asp	Val	Glu	Leu	Leu	Gly	Ala	
			100					105					110			
gta	tgt	aac	aag	att	tgg	tac	ctc	gac	gca	gta	cgc	agc	gaa	gcc	gat	384
Val	Cys	Asn	Lys	Ile	Trp	Tyr	Leu	Asp	Ala	Val	Arg	Ser	Glu	Ala	Asp	
		115					120					125				
gtc	tac	aac	atg	ggc	ttt	agc	aaa	tac	gtc	gat	gca	cgt	gca	ctc	gat	432
Val	Tyr	Asn	Met	Gly	Phe	Ser	Lys	Tyr	Val	Asp	Ala	Arg	Ala	Leu	Asp	
	130					135					140					
gaa	gca	cgc	cga	cgc	cgt	gag	cgc	gca	aac	gcc	gaa	aag	aag	gcc	gga	480
Glu	Ala	Arg	Arg	Arg	Arg	Glu	Arg	Ala	Asn	Ala	Glu	Lys	Lys	Ala	Gly	
145					150				155					160		
gcc	ctc	aag	gac	cag	gct	gca	cgc	ctc	ggc	gcg	aaa	gca	acc	aag	gct	528
Ala	Leu	Lys	Asp	Gln	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Ala	Thr	Lys	Ala	
			165					170					175			
gcc	gca	gct	aag	cag	atg	atc	gcc	cgt	gcg	gaa	cga	atg	atc	gac	aac	576
Ala	Ala	Ala	Lys	Gln	Met	Ile	Ala	Arg	Ala	Glu	Arg	Met	Ile	Asp	Asn	
			180				185						190			
ctc	gac	gaa	atc	cgc	gta	gct	gac	cgc	gcc	gcc	aac	atc	gtt	ttc	cca	624
Leu	Asp	Glu	Ile	Arg	Val	Ala	Asp	Arg	Ala	Ala	Asn	Ile	Val	Phe	Pro	
		195					200					205				
gaa	cca	gca	ccc	tgt	gga	aaa	acc	cca	ctc	aac	gcc	aag	ggc	ctg	acc	672
Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr	
	210					215					220					
aag	atg	tac	ggc	tcc	ctc	gaa	gtc	ttc	gcc	ggc	gtc	gac	cta	gcc	atc	720
Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile	
225					230					235				240		
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggt	gca	ggt	aaa	768
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys	
			245					250						255		
acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggt	gtg	gaa	cgc	acc	gac	ggc	gaa	816
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu	

260	265	270	
ggc ggc atc gtc acc gga tac	ggc ctc aaa atc ggc tac	ttc gcc cag	864
Gly Gly Ile Val Thr Gly Tyr	Gly Leu Lys Ile Gly Tyr	Phe Ala Gln	
275	280	285	
gaa cac gac acc atc gac ccc	gac aaa tcc gtc tgg caa aac	acc atc	912
Glu His Asp Thr Ile Asp Pro	Asp Lys Ser Val Trp Gln Asn	Thr Ile	
290	295	300	
gaa gcc tgc gcc gac gcc gac	caa caa agc ctc cgc agc ctc	ctc gga	960
Glu Ala Cys Ala Asp Ala Asp	Gln Gln Ser Leu Arg Ser Leu	Leu Gly	
305	310	315 320	
tcc ttc atg ttc tcc ggc gaa	caa ctc gac caa cca gca gga	aca ctc	
1008			
Ser Phe Met Phe Ser Gly Glu	Gln Leu Asp Gln Pro Ala Gly	Thr Leu	
325	330	335	
tcc ggc ggt gaa aaa acc cgc	ctc gca ctg gcc acc ctc	gtg tcc tcc	
1056			
Ser Gly Gly Glu Lys Thr Arg	Leu Ala Leu Ala Thr Leu Val	Ser Ser	
340	345	350	
cgc gca aac gtc ctg ctt ctc	gac gag ccc acc aac aac	ctt gac ccg	
1104			
Arg Ala Asn Val Leu Leu Leu	Asp Glu Pro Thr Asn Asn	Leu Asp Pro	
355	360	365	
atc tcc cgc gaa cag gtc ctc	gac gca ctg cgc acc tac	acc ggc gca	
1152			
Ile Ser Arg Glu Gln Val Leu	Asp Ala Leu Arg Thr Tyr	Thr Gly Ala	
370	375	380	
gtc gtc ctg gtt acc cac gac	ccg ggt gca gtc aag gcc	ctt gag cca	
1200			
Val Val Leu Val Thr His Asp	Pro Gly Ala Val Lys Ala	Leu Glu Pro	
385	390	395 400	
gaa cgc gtc atc gtg ctt cct	gat ggc acc gag gat ctt	tgg aat gat	
1248			
Glu Arg Val Ile Val Leu Pro	Asp Gly Thr Glu Asp Leu	Trp Asn Asp	
405	410	415	
cag tac atg gaa atc gtg gaa	ttg gcg taggttctaa	ggctgtttat	
1295			
Gln Tyr Met Glu Ile Val Glu	Leu Ala		
420	425		

gct  
1298

<210> 1104

<211> 425

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1104

Ile	Arg	Lys	Tyr	Ser	Arg	Leu	Glu	Glu	Gln	Phe	Gln	Ser	Leu	Gly	Gly
1				5					10					15	

Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu  
 20 25 30  
 Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln  
 35 40 45  
 Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly  
 50 55 60  
 Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His  
 65 70 75 80  
 Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His  
 85 90 95  
 Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala  
 100 105 110  
 Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp  
 115 120 125  
 Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp  
 130 135 140  
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly  
 145 150 155 160  
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala  
 165 170 175  
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn  
 180 185 190  
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro  
 195 200 205  
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr  
 210 215 220  
 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile  
 225 230 235 240  
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys  
 245 250 255  
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu  
 260 265 270  
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln  
 275 280 285  
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile  
 290 295 300  
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly  
 305 310 315 320  
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu  
 325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser  
 340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro  
 355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala  
 370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro  
 385 390 395 400

Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp  
 405 410 415

Gln Tyr Met Glu Ile Val Glu Leu Ala  
 420 425

&lt;210&gt; 1105

&lt;211&gt; 613

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)

&lt;223&gt; RXN03171

&lt;400&gt; 1105

atactttgtt ggactggaaa agtggccgtt tggttccctc caagcccaaa ttcgcccgcg 60

cggctcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115  
 Met Asp Ile Thr Ile  
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115  
 cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130  
 acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145  
 gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165  
 gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
 170

&lt;210&gt; 1106

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1106

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr  
 1 5 10 15  
 Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
 20 25 30  
 Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
 35 40 45  
 Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
 50 55 60  
 Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
 65 70 75 80  
 Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
 85 90 95  
 Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
 100 105 110  
 Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
 115 120 125  
 Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
 130 135 140  
 Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
 145 150 155 160  
 Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser  
 165 170

&lt;210&gt; 1107

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<211> 613
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(613)
<223> FRXA02857
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<400>	1107
atacttttggtt ggactggaaa agtggccggtt tggttcacct caagccccaa ttcgcccgcg	60
cgggtccttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc Met Asp Ile Thr Ile	115
	1 5
gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu	163
	10 15 20
cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala	211
	25 30 35
atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp	259
	40 45 50
acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro	307
	55 60 65
ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro	355
	70 75 80 85
gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala	403
	90 95 100
cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro	451
	105 110 115
cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala	499
	120 125 130
acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly	547
	135 140 145
gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val	595
	150 155 160 165
gac gca ttg gcg gaa tct Asp Ala Leu Ala Glu Ser	613
	170

<210> 1108  
 <211> 171  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1108

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Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
 1           5           10           15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
          20           25           30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
          35           40           45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
          50           55           60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
          65           70           75           80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
          85           90           95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
          100          105          110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
          115          120          125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
          130          135          140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
          145          150          155          160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
          165          170
  
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<210> 1109  
 <211> 424  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> RXN00450

<400> 1109

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tttgcgatga catggatttg gatccttccg aacaattgct gcgcatcgcg gaagaactcg 60

gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
                               Val Gly Val Leu Pro
                               1           5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
          10           15           20
  
```

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211  
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val  
 25 30 35  
 att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259  
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg  
 40 45 50  
 gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307  
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg  
 55 60 65  
 cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr  
 70 75 80 85  
 gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403  
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val  
 90 95 100  
 ggt gct cga atc gga cgc atc 424  
 Gly Ala Arg Ile Gly Arg Ile  
 105

&lt;210&gt; 1110

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1110

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg  
 1 5 10 15  
 Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
 20 25 30  
 Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
 35 40 45  
 Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
 50 55 60  
 Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
 65 70 75 80  
 Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
 85 90 95  
 Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile  
 100 105

&lt;210&gt; 1111

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(418)



&lt;223&gt; FRXA00450

&lt;400&gt; 1111

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tttgcgatga catggatttg gatccttccg aacaattgct gcgcacgcgc gaagaactcg 60

gttttgataa tgatctggct cgggtgggtgg gattcgacta gtg ggc gtt tta cct 115
                                   Val Gly Val Leu Pro
                                   1           5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
              10              15              20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
              25              30              35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
              40              45              50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
              55              60              65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
              70              75              80              85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
              90              95              100

ggt gct cga atc gga
Gly Ala Arg Ile Gly
              105

```

&lt;210&gt; 1112

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1112

```

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
  1           5           10           15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
              20              25              30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
              35              40              45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
              50              55              60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
              65              70              75              80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
              85              90              95

```

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly  
 100 105

<210> 1113

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00465

<400> 1113

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caagcgcctac cagcgttgat gcgagggttg agcgcctaac atg act gaa gat gac 115  
 Met Thr Glu Asp Asp  
 1 5

tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163  
 Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys  
 10 15 20

cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211  
 Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val Asp Pro Phe Gly Ala  
 25 30 35

gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259  
 Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys  
 40 45 50

cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307  
 His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala  
 55 60 65

tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355  
 Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala  
 70 75 80 85

atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403  
 Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys  
 90 95 100

gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451  
 Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala  
 105 110 115

gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499  
 Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn  
 120 125 130

ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547  
 Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu  
 135 140 145

ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592  
 Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu  
 150 155 160

tagcgctggg catgtgactt taa

615

&lt;210&gt; 1114

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1114

Met	Thr	Glu	Asp	Asp	Leu	Asp	Leu	Leu	His	Arg	Thr	Val	Glu	Leu	Ala
1				5					10					15	

Thr	Gln	Ala	Leu	Lys	Gln	Gly	Asn	Ser	Pro	Tyr	Gly	Ser	Leu	Leu	Val
			20					25					30		

Asp	Pro	Phe	Gly	Ala	Val	Val	Phe	Glu	Asp	His	Asn	Arg	Asp	Ala	Asp
		35					40					45			

Gly	Asp	Leu	Thr	Lys	His	Pro	Glu	Phe	Ala	Ile	Ala	Lys	Tyr	Ala	Ile
	50					55					60				

Glu	Asn	Tyr	Ser	Ala	Ser	Glu	Arg	Ala	Ala	Cys	Thr	Val	Tyr	Thr	Ser
65					70					75					80

Thr	Glu	His	Cys	Ala	Met	Cys	Ala	Gly	Ala	His	Ala	Trp	Ala	Gly	Leu
			85						90					95	

Gly	Lys	Ile	Tyr	Cys	Ala	Thr	Thr	Gly	Gly	Gln	Thr	Ala	Ala	Trp	Tyr
		100						105					110		

Ala	Lys	Trp	Gly	Ala	Glu	Ser	Gly	Pro	Leu	Asn	Pro	Ile	Ser	Ala	Asp
		115					120					125			

Lys	Ile	Ser	Pro	Asn	Ile	Ser	Ile	Glu	Gly	Pro	Ala	Ser	Arg	Phe	Glu
	130				135						140				

Glu	Val	Leu	Tyr	Glu	Leu	His	Arg	Trp	Phe	Tyr	Leu	Gly	Gln	Ser	Pro
145					150					155					160

Asn Lys Ala Leu

&lt;210&gt; 1115

&lt;211&gt; 1083

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1060)

&lt;223&gt; RXA00717

&lt;400&gt; 1115

aagcatcagt taaagccccg actattaaaa tctcctaaaa taggctagaa ttcacgggat 60

tcaatttcat	acgttttctc	tcaagattaa	ggacacttac	gtg	acc	cca	ccc	gct	115
				Val	Thr	Pro	Pro	Ala	
				1				5	

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga	163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly	
10 15 20	
tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac	211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn	
25 30 35	
aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct	259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala	
40 45 50	
aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg	307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met	
55 60 65	
ggt ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg	355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val	
70 75 80 85	
ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att	403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile	
90 95 100	
gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc	451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly	
105 110 115	
gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc	499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg	
120 125 130	
atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt	547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg	
135 140 145	
ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt	595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly	
150 155 160 165	
gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc	643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val	
170 175 180	
ggt cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat	691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp	
185 190 195	
ggt gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag	739
Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys	
200 205 210	
act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc	787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser	
215 220 225	
gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac	835
Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp	
230 235 240 245	
ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc	883

Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile  
 250 255 260  
 gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931  
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu  
 265 270 275  
 ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979  
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val  
 280 285 290  
 cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct  
 1027  
 Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser  
 295 300 305  
 gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg  
 1080  
 Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 310 315 320  
 cct  
 1083  
 <210> 1116  
 <211> 320  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 1116  
 Val Thr Pro Pro Ala Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser  
 1 5 10 15  
 Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly  
 20 25 30  
 Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile  
 35 40 45  
 Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp  
 50 55 60  
 Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val  
 65 70 75 80  
 Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His  
 85 90 95  
 Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile  
 100 105 110  
 Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg  
 115 120 125  
 Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val  
 130 135 140  
 Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly  
 145 150 155 160

Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln  
 165 170 175

Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu  
 180 185 190

Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys  
 195 200 205

Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr  
 210 215 220

Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly  
 225 230 235 240

Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys  
 245 250 255

Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg  
 260 265 270

Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr  
 275 280 285

Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg  
 290 295 300

Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 305 310 315 320

&lt;210&gt; 1117

&lt;211&gt; 978

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(955)

&lt;223&gt; RXA01894

&lt;400&gt; 1117

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aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163  
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly  
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 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly

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gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly 120 125 130			499
agc ttc gct gcg atg ctg tct ctg atg caa aac aat tcc atc ccg ggt Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly 135 140 145			547
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tct gat gtg Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val 150 155 160 165			595
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cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala 215 220 225			787
acg ttg ggt gac ttg gtt gag tct cag ttc aaa cgc gat ttg ggc atc Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile 230 235 240 245			835
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&lt;210&gt; 1118

&lt;211&gt; 285

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1118

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Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
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Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
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Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
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Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
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Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
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Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
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Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
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Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
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His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
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Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
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Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
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 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg  
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 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr  
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 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys  
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 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly  
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 150 155 160 165  
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 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala

170										175					180					
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Pro	Glu	Met	Leu	Ile	Ala	Asp	Ile	Asp	Val	Ser	Gly	Leu	Ala	Lys	Ile					
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Thr	Ser	Trp	Gln	Asp	Gly	Pro	Gly	Lys	Leu	Glu	Gln	Trp	Glu	Val	Leu					
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Met Cys Glu Arg Pro  
1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
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Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259  
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val  
40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307  
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala  
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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355  
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ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403  
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370 375 380

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 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala  
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acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595  
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 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123



Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
440 445 450

tcc cat ggc aca ggc tgt tgg ctc tct gcg tca ctt gcc acc aag atc  
1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
455 460 465

gcc gcc ggc gaa agc gtg gaa  
1528

Ala Ala Gly Glu Ser Val Glu  
470 475

<210> 1124

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1124

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
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Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
 35 40 45  
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

355	360	365	
Glu Ser Leu Arg Arg Leu	Ala Val His Val Asp	Val Val Thr Pro Asn	
370	375	380	
Ile Pro Glu Leu Ala Val	Leu Cys Asp Ser Ala	Pro Ala Ile Thr Met	
385	390	395	400
Asp Glu Ala Ile Ala Gln	Ala Gln Gly Phe Ala	Arg Thr His Asp Thr	
405	410	415	
Ile Val Ile Val Lys Gly	Gly His Leu Thr Gly	Ala Leu Ala Asp Asn	
420	425	430	
Ala Val Val Arg Pro Asp	Gly Ser Val Phe Gln	Val Glu Asn Leu Arg	
435	440	445	
Val Asn Thr Thr Asn Ser	His Gly Thr Gly Cys	Ser Leu Ser Ala Ser	
450	455	460	
Leu Ala Thr Lys Ile Ala	Ala Gly Glu Ser Val	Glu	
465	470	475	
<210> 1125			
<211> 795			
<212> DNA			
<213> Corynebacterium glutamicum			
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<222> (101)..(772)			
<223> RXN01617			
<400> 1125			
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tgtttatggc attgggtcca	tcacatgctt ggggtggcctt	ttg atc cta aag aca	115
		Leu Ile Leu Lys Thr	
		1 5	
act gga atc acc gtt ttg	tcc cgg ttt gat gcg	cag gtt atc gct aat	163
Thr Gly Ile Thr Val Leu	Ser Arg Phe Asp Ala	Gln Val Ile Ala Asn	
10	15	20	
cag att gag gcc gcc acc	gca gcg cac gat ctt	gat gtg gtg aag atc	211
Gln Ile Glu Ala Ala Thr	Ala Ala His Asp Leu	Asp Val Val Lys Ile	
25	30	35	
ggt atg ttg ggt act cct	gca acg atc gat act	gtg gca acc gct ttg	259
Gly Met Leu Gly Thr Pro	Ala Thr Ile Asp Thr	Val Ala Thr Ala Leu	
40	45	50	
gag gaa aac agc ttc aag	cac gtt gtc cta gac	ccg gta ctg atc tgc	307
Glu Glu Asn Ser Phe Lys	His Val Val Leu Asp	Pro Val Leu Ile Cys	
55	60	65	
aag ggc cag gag ccc ggc	gcg gca ctt gat act	gac act gcc ctt cgc	355
Lys Gly Gln Glu Pro Gly	Ala Ala Leu Asp Thr	Asp Thr Ala Leu Arg	
70	75	80	85

gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403  
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu  
                     90                    95                    100

gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451  
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu  
                     105                    110                    115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499  
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val  
                     120                    125                    130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547  
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu  
                     135                    140                    145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595  
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp  
                     150                    155                    160                    165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643  
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala  
                     170                    175                    180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691  
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys  
                     185                    190                    195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739  
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro  
                     200                    205                    210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc 792  
 Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
                     215                    220

cct 795

<210> 1126  
 <211> 224  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1126  
 Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala  
     1                    5                    10                    15

Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu  
                     20                    25                    30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
                     35                    40                    45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
                     50                    55                    60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
                     65                    70                    75                    80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr

85										90					95				
Pro	Asn	Asn	Phe	Glu	Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu				
			100					105					110						
Thr	Ile	Asp	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly				
		115				120						125							
Pro	Gln	Tyr	Val	Val	Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn				
		130				135					140								
Ala	Val	Asp	Val	Leu	Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu				
145					150					155					160				
Pro	Lys	Ile	Gly	Asp	Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala				
			165						170					175					
Ala	Val	Ile	Thr	Ala	Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala				
			180					185						190					
Val	Thr	Thr	Ala	Lys	Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val				
		195					200						205						
Ala	Ser	Asn	Ala	Pro	Phe	Thr	Ser	Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys				
		210				215						220							

&lt;210&gt; 1127

&lt;211&gt; 638

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(615)

&lt;223&gt; FRXA01617

&lt;400&gt; 1127

gct	aat	cag	att	gag	gcc	gcc	acc	gca	gcg	cac	gat	ctt	gat	gtg	gtg				48
Ala	Asn	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu	Asp	Val	Val				
1				5					10					15					
aag	atc	ggt	atg	ttg	ggt	act	cct	gca	acg	atc	gat	act	gtg	gca	acc				96
Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr				
			20					25					30						
gct	ttg	gag	gaa	aac	agc	ttc	aag	cac	ggt	gtc	cta	gac	ccg	gta	ctg				144
Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu				
			35				40					45							
atc	tgc	aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc				192
Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala				
		50				55					60								
ctt	cgc	gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	ggt	act	cca	aac	aac				240
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn				
		65				70					75				80				

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Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
                20                          25                  30  
  
Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu  
        35                                40                    45  
  
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala  
    50                      55                        60  
  
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn  
  65                       70               75                  80  
  
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp  
                85                                90                 95  
  
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr  
      100                            105              110
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Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile  
130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
195 200 205

<210> 1129

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXC01600

<400> 1129

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tttggagctg cgtgtccacc cttagatcta caatgtgata atg gtt tcg aag atg 115  
Met Val Ser Lys Met  
1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163  
His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu  
10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211  
Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro  
25 30 35

ggg ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259  
Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val  
40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307  
Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr  
55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355  
Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu  
70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403  
Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met  
90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451  
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu  
 105 110 115

att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499  
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala  
 120 125 130

cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547  
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu  
 135 140 145

gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595  
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met  
 150 155 160 165

gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643  
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met  
 170 175 180

gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691  
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr  
 185 190 195

gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739  
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala  
 200 205 210

cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789  
 His Gly Ile Val Pro Asp Met Lys Lys Leu  
 215 220

aaa 792

&lt;210&gt; 1130

&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1130

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr  
 1 5 10 15

Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp  
 20 25 30

Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu  
 35 40 45

His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala  
 50 55 60

Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu  
 65 70 75 80

Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala  
 85 90 95

Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser  
 100 105 110



Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val  
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val  
 130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His  
 145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala  
 165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser  
 180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala  
 195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu  
 210 215 220

&lt;210&gt; 1131

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(703)

&lt;223&gt; RXC01622

&lt;400&gt; 1131

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gccatcgcag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115  
 Met Ser Asp Phe Tyr  
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163  
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly  
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211  
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg  
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259  
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val  
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307  
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu  
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355  
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro  
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403

Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val  
 90 95 100  
 gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451  
 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val  
 105 110 115  
 cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499  
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu  
 120 125 130  
 ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547  
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu  
 135 140 145  
 aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595  
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro  
 150 155 160 165  
 tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643  
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met  
 170 175 180  
 cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691  
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp  
 185 190 195  
 cct tca gat aat tagatgagtt ccgaaaattt aaa 726  
 Pro Ser Asp Asn  
 200

&lt;210&gt; 1132

&lt;211&gt; 201

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1132

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn  
 1 5 10 15  
 Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser  
 20 25 30  
 Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala  
 35 40 45  
 Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala  
 50 55 60  
 Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu  
 65 70 75 80  
 Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val  
 85 90 95  
 Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu  
 100 105 110  
 Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val  
 115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp  
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val  
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile  
 165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser  
 180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn  
 195 200

<210> 1133

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 1133

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115  
 Val Ser Lys Ile Ser  
 1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163  
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val  
 10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211  
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg  
 25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259  
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro  
 40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307  
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala  
 55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355  
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly  
 70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403  
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg  
 90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451  
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile  
 105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499  
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr  
120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547  
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu  
135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595  
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu  
150 155 160 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt 643  
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe  
170 175 180

gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat 691  
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn  
185 190 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt 739  
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly  
200 205 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat 787  
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp  
215 220 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg 835  
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu  
230 235 240 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg 883  
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val  
250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931  
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala  
265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979  
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp  
280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg  
1027  
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu  
295 300 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg  
1075  
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val  
310 315 320 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg  
1123  
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala  
330 335 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac  
 1171  
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn  
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg  
 1219  
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala  
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt  
 1267  
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser  
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga  
 1315  
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg  
 1363  
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu  
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act  
 1411  
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc  
 1459  
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag  
 1507  
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
 455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca  
 1555  
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
 470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg  
 1603  
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
 490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat  
 1651  
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
 505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac  
 1699  
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
 520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat  
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg  
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
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gtt gcg tac tgatggagct gttcttcccg cgc  
1827

Val Ala Tyr

<210> 1134

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 1134

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400  
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro

1545



gat

555

&lt;210&gt; 1136

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1136

Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly  
 1 5 10 15

Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser  
 20 25 30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly  
 35 40 45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg  
 50 55 60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys  
 65 70 75 80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser  
 85 90 95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser  
 100 105 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu  
 115 120 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser  
 130 135 140

&lt;210&gt; 1137

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(898)

&lt;223&gt; RXC02207

&lt;400&gt; 1137

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ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115  
 Met Arg Arg Arg Ser  
 1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163  
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala  
 10 15 20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg	211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met	
25 30 35	
ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc	259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly	
40 45 50	
caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt	307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly	
55 60 65	
gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc	355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val	
70 75 80 85	
tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa	403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln	
90 95 100	
tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc	451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala	
105 110 115	
gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg	499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu	
120 125 130	
cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat	547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp	
135 140 145	
cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc	595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg	
150 155 160 165	
gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag	643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln	
170 175 180	
ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc	691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr	
185 190 195	
tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt	739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg	
200 205 210	
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt	787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly	
215 220 225	
ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att	835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile	
230 235 240 245	
gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc	883
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro	
250 255 260	

cac cga cga gga acc  
His Arg Arg Gly Thr  
265

898

&lt;210&gt; 1138

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1138

Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu  
1 5 10 15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr  
20 25 30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala  
35 40 45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met  
50 55 60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu  
65 70 75 80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu  
85 90 95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe  
100 105 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro  
115 120 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala  
130 135 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu  
145 150 155 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala  
165 170 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp  
180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp  
195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val  
210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu  
225 230 235 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu  
245 250 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr  
260 265

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<210> 1139
<211> 891
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(868)  
<223> RXA00347
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<400> 1139																
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				Met	Thr	Leu	Thr	Ile	5							
				1												
gag	gaa	atc	gcc	aag	acc	aaa	aag	ctt	ttg	gtt	gtg	tcc	gat	ttt	gat	163
Glu	Glu	Ile	Ala	Lys	Thr	Lys	Lys	Leu	Leu	Val	Val	Ser	Asp	Phe	Asp	
			10						15					20		
gga	acc	atc	gca	gga	ttt	agc	aag	gac	gct	tac	aac	gtt	cct	atc	aac	211
Gly	Thr	Ile	Ala	Gly	Phe	Ser	Lys	Asp	Ala	Tyr	Asn	Val	Pro	Ile	Asn	
			25					30					35			
cag	aaa	tcc	ctc	aag	gcg	gta	aaa	gac	ctc	tcc	caa	caa	gca	gac	act	259
Gln	Lys	Ser	Leu	Lys	Ala	Val	Lys	Asp	Leu	Ser	Gln	Gln	Ala	Asp	Thr	
		40					45					50				
gat	gtt	gtc	att	ttg	tcg	gga	cgt	cac	ctg	gag	gga	ttg	aag	acg	gtt	307
Asp	Val	Val	Ile	Leu	Ser	Gly	Arg	His	Leu	Glu	Gly	Leu	Lys	Thr	Val	
	55					60					65					
ctt	gat	ctt	ggt	cag	tac	gac	atc	acc	atg	gtg	ggt	tca	cac	ggt	tct	355
Leu	Asp	Leu	Gly	Gln	Tyr	Asp	Ile	Thr	Met	Val	Gly	Ser	His	Gly	Ser	
	70				75				80						85	
gag	gat	tcc	tcc	cgc	ccg	cgt	acc	ctc	act	cct	gaa	gag	gta	gct	cgc	403
Glu	Asp	Ser	Ser	Arg	Pro	Arg	Thr	Leu	Thr	Pro	Glu	Glu	Val	Ala	Arg	
				90					95					100		
ctc	gcc	aag	att	gaa	gca	gat	ctg	gaa	aag	atc	gtc	gac	ggc	atc	gaa	451
Leu	Ala	Lys	Ile	Glu	Ala	Asp	Leu	Glu	Lys	Ile	Val	Asp	Gly	Ile	Glu	
			105					110					115			
ggc	gca	ttc	gtg	gag	atc	aag	cct	ttc	cac	cgc	gtg	ctg	cac	ttc	atc	499
Gly	Ala	Phe	Val	Glu	Ile	Lys	Pro	Phe	His	Arg	Val	Leu	His	Phe	Ile	
		120					125					130				
cgt	gtt	tcc	gac	aag	gac	aaa	gtc	caa	gga	atc	ctc	gcc	caa	gca	gca	547
Arg	Val	Ser	Asp	Lys	Asp	Lys	Val	Gln	Gly	Ile	Leu	Ala	Gln	Ala	Ala	
		135				140					145					
cac	gta	gac	tct	tcc	ggc	ctg	aag	gtt	act	aac	ggc	aag	agc	atc	atc	595
His	Val	Asp	Ser	Ser	Gly	Leu	Lys	Val	Thr	Asn	Gly	Lys	Ser	Ile	Ile	
					155				160					165		
gaa	tac	tcc	atc	agc	tcc	acc	acc	aag	ggc	acc	tgg	ctg	aag	gaa	tac	643
Glu	Tyr	Ser	Ile	Ser	Ser	Thr	Thr	Lys	Gly	Thr	Trp	Leu	Lys	Glu	Tyr	

170	175	180	
gtt gac cgc acc gag ccc act ggt gtg att ttc ctc ggc gat gac acc			691
Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe Leu Gly Asp Asp Thr			
185	190	195	
acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta			739
Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu			
200	205	210	
acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac			787
Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp			
215	220	225	
gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc			835
Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg			
230	235	240	245
atg cag tat gcg gaa agc gtg cga ttg ggg att taagagagcc taaacgcacg			888
Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile			
250	255		

aaa

891

&lt;210&gt; 1140

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1140

Met Thr Leu Thr Ile Glu Glu Ile Ala Lys Thr Lys Lys Leu Leu Val
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Val Ser Asp Phe Asp Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr
20                      25                      30

Asn Val Pro Ile Asn Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser
35                      40                      45

Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu
50                      55                      60

Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val
65                      70                      75                      80

Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro
85                      90                      95

Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile
100                      105                      110

Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg
115                      120                      125

Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile
130                      135                      140

Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn
145                      150                      155                      160

Gly Lys Ser Ile Ile Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr  
 165 170 175

Trp Leu Lys Glu Tyr Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe  
 180 185 190

Leu Gly Asp Asp Thr Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn  
 195 200 205

Asp Asp Arg Ala Leu Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala  
 210 215 220

Lys Thr Arg Val Asp Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys  
 225 230 235 240

Leu Ala Tyr His Arg Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile  
 245 250 255

<210> 1141  
 <211> 2556  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2533)  
 <223> RXN01239

<400> 1141  
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 Met Ala Arg Pro Ile  
 1 5

tcc gca acg tac agg ctt caa atg cga gga cct caa gca gat agc gcc 163  
 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala  
 10 15 20

ggg cgt tca ttt ggt ttt gcg cag gcc aaa gcc cag ctt ccc tat ctg 211  
 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu  
 25 30 35

aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259  
 Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala  
 40 45 50

atg cca gat tcc aat cat ggc tac gat gtc att gat ccc acc acc atc 307  
 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile  
 55 60 65

aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct 355  
 Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala  
 70 75 80 85

aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403  
 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His

90	95	100	
tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu 105 110 115			451
aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp 120 125 130			499
cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly 135 140 145			547
gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu 150 155 160 165			595
aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr 170 175 180			643
gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu 185 190 195			691
cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val 200 205 210			739
aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His 215 220 225			787
act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly 230 235 240 245			835
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 Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile  
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 Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg  
 65 70 75 80  
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 85 90 95  
 Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp

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Met	Pro	Ile	Leu	Gly	Ala	Glu	Gly	Asp	Glu	Asp	Lys	Leu	Glu	Phe	Ala	
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Thr	Glu	Glu	Ser	Leu	Lys	Arg	Val	Val	Ala	Gln	Gln	Glu	Leu	Ala	Ala	
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Glu	Ile	Leu	Arg	Leu	Ala	Arg	Ala	Met	Arg	Arg	Asp	Asn	Phe	Ser	Thr	
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Leu	Val	Ala	Ala	Met	Pro	Val	Tyr	Arg	Ala	Asp	Tyr	Ile	Ser	Leu	Ser	
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Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
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2467

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Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr  
115 120 125

Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly  
130 135 140

Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala  
145 150 155 160

Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro  
 165 170 175  
 Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg  
 180 185 190  
 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg  
 195 200 205  
 Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro  
 210 215 220  
 Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu  
 225 230 235 240  
 Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp  
 245 250 255  
 Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg  
 260 265 270  
 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro  
 275 280 285  
 Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu  
 290 295 300  
 Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu  
 305 310 315 320  
 Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser  
 325 330 335  
 Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala  
 340 345 350  
 Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr  
 355 360 365  
 Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu  
 370 375 380  
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 385 390 395 400  
 Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser  
 405 410 415  
 Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly  
 420 425 430  
 Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys  
 435 440 445  
 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu  
 450 455 460  
 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu  
 465 470 475 480

Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met  
 485 490 495  
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala  
 500 505 510  
 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val  
 515 520 525  
 Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser  
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 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile  
 545 550 555 560  
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile  
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 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe  
 580 585 590  
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser  
 595 600 605  
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val  
 610 615 620  
 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile  
 625 630 635 640  
 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp  
 645 650 655  
 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu  
 660 665 670  
 Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp  
 675 680 685  
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser  
 690 695 700  
 Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His  
 705 710 715 720  
 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile  
 725 730 735  
 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr  
 740 745 750  
 Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr  
 755 760 765  
 Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
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805

810

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1930)  
<223> RXA02645
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Met Leu Lys Asp Leu																115
1 5																
acc ggc ctg agg gag ttg gta ttg cgt gag atg tgc cat agc atc tca																163
Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met Cys His Ser Ile Ser																
10 15 20																
cat ctt agc tcg cca acc ggc agc att ttc act agc ctg gtg gcc atg																211
His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met																
25 30 35																
ttg acc tcg caa agc ttt tca gtg tgg gct cca ctt ccc cac gat gta																259
Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val																
40 45 50																
cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc																307
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly																
55 60 65																
agc tgg tgg cgc gcc gag atc gcg ccc aag gcc ggc gat cgt tac ggt																355
Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly																
70 75 80 85																
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Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro																
90 95 100																
cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc																451
Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser																
105 110 115																
gat gat tcc tat ctg tgg ggt gac cag cag tgg act ggc cga att ctc																499
Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu																
120 125 130																
cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat																547
Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly Thr Phe Ser Glu Asp																
135 140 145																
gga acg ttt gag gga gtc gtc gac aag ctt cct tat ctg cgc gac ctc																595
Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro Tyr Leu Arg Asp Leu																
150 155 160 165																
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Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln Pro Phe Gly Gly Asn	
170	175 180
cgc aat tgg ggc tac gac ggg gtg ctg tgg cac gcc gtc cat gca ggc	691
Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His Ala Val His Ala Gly	
185	190 195
tac ggc ggt ccg gcg ggc ttg aaa aag ctt atc gac gcc tcc cac cag	739
Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile Asp Ala Ser His Gln	
200	205 210
gcc ggc atc gcc gtc tac tta gac gtc gtg tac aac cac ttc ggc ccc	787
Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr Asn His Phe Gly Pro	
215	220 225
gac ggc aac tac aac ggg caa ttt ggc ccc tac acc tct ggc ggc agc	835
Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr Thr Ser Gly Gly Ser	
230	235 240 245
acc ggc tgg ggc gac gtg gtc aac atc aac ggc cat gat tca gat gaa	883
Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly His Asp Ser Asp Glu	
250	255 260
gtc cgc aat tat att ctc gac gcc gca cgc cag tgg ttc gaa gat ttt	931
Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln Trp Phe Glu Asp Phe	
265	270 275
cac gtt gat ggc ctc cgc ctc gat gcg gtg cat tct ctc gat gat cgc	979
His Val Asp Gly Leu Arg Leu Asp Ala Val His Ser Leu Asp Asp Arg	
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ggc gcc tat tcc cta ctt gcg cag ctg acc atg gtg gcc gag gat gtc	
1027	
Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met Val Ala Glu Asp Val	
295	300 305
tcc gca caa aca ggc atc cca cgc tca ttg att gca gaa tct gaa ctc	
1075	
Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile Ala Glu Ser Glu Leu	
310	315 320 325
aat gac ccc aag ttc gtt acc tcc cgc gag gcc ggc ggt ttt ggc ctg	
1123	
Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala Gly Gly Phe Gly Leu	
330	335 340
gat gca cag tgg gtt gac gat atc cac cac gcc ctc cat gcc ctc gtt	
1171	
Asp Ala Gln Trp Val Asp Asp Ile His His Ala Leu His Ala Leu Val	
345	350 355
tct ggc gaa cgc aat ggt tat tac agc gat ttc gga tct gtc gac aca	
1219	
Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe Gly Ser Val Asp Thr	
360	365 370
tta gcc aaa acc ctg cgt gaa gta ttt gaa cac acc gga aac tac tcc	
1267	
Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His Thr Gly Asn Tyr Ser	
375	380 385

gag ctg att tac agc ttc act tcc ccc acc gtc acc gac acc tcc aca  
1891

Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val Thr Asp Thr Ser Thr  
585 590 595

acc ctt cag ccg tgg ggc ttt gcg atc ctg acc cga aac tagaaaaagg  
1940

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1953

<210> 1146

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 1146

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Ser Leu Val Ala Met Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro  
35 40 45

Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met  
50 55 60

His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala  
65 70 75 80

Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys  
85 90 95

Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly  
100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp  
115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly  
130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro  
145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln  
165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His  
180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile  
195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr  
210 215 220

acg tac cgc gga cgc aac cac ggc cgc cct gtg cac ccc gat atc acc  
 1315  
 Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val His Pro Asp Ile Thr  
 390 395 400 405  
  
 cct gcc tcg cgc ttt gtc acc tac acc acc acc cat gat cag acc ggc  
 1363  
 Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr His Asp Gln Thr Gly  
 410 415 420  
  
 aac cgc gca atc ggc gac cgt cct tcc acg act ctc acc ccg gaa cag  
 1411  
 Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr Leu Thr Pro Glu Gln  
 425 430 435  
  
 cag gtg ttg aag gca gcc att atc tac agc tcg ccg tat acc ccg atg  
 1459  
 Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser Pro Tyr Thr Pro Met  
 440 445 450  
  
 ttg ttt atg ggt gaa gaa ttc gga gcc acc acc cca ttc gcc ttc ttt  
 1507  
 Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr Pro Phe Ala Phe Phe  
 455 460 465  
  
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 1555  
 Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu Thr Ser Glu Gly Arg  
 470 475 480 485  
  
 aaa cgg gaa ttc gca cgc ctt ggc tgg aac gcc gac gac atc ccc tcc  
 1603  
 Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser  
 490 495 500  
  
 ccc gag ctg gaa tcc acc ttc acc tcc tcc aaa ctc gat tgg gag ttc  
 1651  
 Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe  
 505 510 515  
  
 act gcg gag cag cgc cgc atc aac gac gct tac aag cag ctg ttg cac  
 1699  
 Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr Lys Gln Leu Leu His  
 520 525 530  
  
 ctg cgg cac acc ttg ggc ttc tcc caa cca aac ttg ctc aca ctc gag  
 1747  
 Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn Leu Leu Thr Leu Glu  
 535 540 545  
  
 gtt gag cac ggc gag aac tgg cta tcg atg gcc aat ggt cgc ggc cga  
 1795  
 Val Glu His Gly Glu Asn Trp Leu Ser Met Ala Asn Gly Arg Gly Arg  
 550 555 560 565  
  
 att ctg gcg aat ttc tcc gac gac acc atc acc gtc ccg ctt ggc ggc  
 1843  
 Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr Val Pro Leu Gly Gly  
 570 575 580

Asn His Phe Gly Pro Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr  
 225 230 235 240  
 Thr Ser Gly Gly Ser Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly  
 245 250 255  
 His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln  
 260 265 270  
 Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His  
 275 280 285  
 Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met  
 290 295 300  
 Val Ala Glu Asp Val Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile  
 305 310 315 320  
 Ala Glu Ser Glu Leu Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala  
 325 330 335  
 Gly Gly Phe Gly Leu Asp Ala Gln Trp Val Asp Asp Ile His His Ala  
 340 345 350  
 Leu His Ala Leu Val Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe  
 355 360 365  
 Gly Ser Val Asp Thr Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His  
 370 375 380  
 Thr Gly Asn Tyr Ser Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val  
 385 390 395 400  
 His Pro Asp Ile Thr Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr  
 405 410 415  
 His Asp Gln Thr Gly Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr  
 420 425 430  
 Leu Thr Pro Glu Gln Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser  
 435 440 445  
 Pro Tyr Thr Pro Met Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr  
 450 455 460  
 Pro Phe Ala Phe Phe Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu  
 465 470 475 480  
 Thr Ser Glu Gly Arg Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala  
 485 490 495  
 Asp Asp Ile Pro Ser Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys  
 500 505 510  
 Leu Asp Trp Glu Phe Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr  
 515 520 525  
 Lys Gln Leu Leu His Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn  
 530 535 540



Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala  
545 550 555 560

Asn Gly Arg Gly Arg Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr  
565 570 575

Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val  
580 585 590

Thr Asp Thr Ser Thr Thr Leu Gln Pro Trp Gly Phe Ala Ile Leu Thr  
595 600 605

Arg Asn  
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<210> 1147

<211> 832

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(832)

<223> RXN02355

<400> 1147

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Met Ser Ser Ile Ser  
1 5

cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163  
Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile  
10 15 20

gca ctg gcc ggt tgt agt tca gac tca agc tcc gac tcc aca gat tcc 211  
Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser  
25 30 35

acc gct agc gaa ggc gca gac agc cgc ggc ccc atc acc ttt gcg atg 259  
Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met  
40 45 50

ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307  
Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn  
55 60 65

gaa gcc cac ccc gat gag cag gta acg ctc aac gaa ctc gcc ggt gaa 355  
Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn Glu Leu Ala Gly Glu  
70 75 80 85

gcc gac gcg cag cgc gaa acc ctc gtg caa tcc ctg cag gcc ggc aac 403  
Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser Leu Gln Ala Gly Asn  
90 95 100

tct gac tac gac gtc atg gcg ctc gac gtc atc tgg acc gca gac ttc 451  
Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe  
105 110 115

gcg gca aac caa tgg ctc gca cca ctt gaa ggc gac ctc gag gta gac 499  
 Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly Asp Leu Glu Val Asp  
 120 125 130

acc tcc gga ctg ctg caa tcc acc gtg gat tcc gca acc tac aac ggc 547  
 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly  
 135 140 145

acc ctc tac gca ctg cca cag aac acc aac ggc cag cta ctg ttc cgc 595  
 Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly Gln Leu Leu Phe Arg  
 150 155 160 165

aac acc gaa atc atc cca gaa gca cca gca aac tgg gct gac ctc gtg 643  
 Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn Trp Ala Asp Leu Val  
 170 175 180

gaa tcc tgc acg ctt gct gaa gaa gca ggc gtt gat tgc ctg acc act 691  
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 185 190 195

cag ctc aag cag tac gaa ggc ctt tca gtg aac acc atc ggc ttc atc 739  
 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile  
 200 205 210

gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787  
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg  
 215 220 225

aga cag cac gac ggc aag gca ggc ctt caa gcg ctt gtc gac ggc 832  
 Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala Leu Val Asp Gly  
 230 235 240

&lt;210&gt; 1148

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1148

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Leu Leu Ala Ala Ile Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser  
 20 25 30

Asp Ser Thr Asp Ser Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro  
 35 40 45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile  
 50 55 60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn  
 65 70 75 80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser  
 85 90 95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile  
 100 105 110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115	120	125
Asp Leu Glu Val Asp Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser		
130	135	140
Ala Thr Tyr Asn Gly Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly		
145	150	155
Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn		
165	170	175
Trp Ala Asp Leu Val Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val		
180	185	190
Asp Cys Leu Thr Thr Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn		
195	200	205
Thr Ile Gly Phe Ile Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp		
210	215	220
Gly Lys Arg His Arg Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala		
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		240
Leu Val Asp Gly		

<210> 1149  
 <211> 609  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(586)  
 <223> RXN02909

<400> 1149  
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 Met Asn Arg Ala Arg  
 1 5  
 atc gcg acc ata ggc gtt ctt ccg ctt gct tta ctg ctg gcg tcc tgt 163  
 Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Leu Ala Ser Cys  
 10 15 20  
 ggt tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat 211  
 Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn  
 25 30 35  
 att tac acc gat cca gat gag tcg aat tcg atc agt aat ctt gtc att 259  
 Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile  
 40 45 50  
 tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act 307  
 Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Leu Ser Gly Phe Thr  
 55 60 65  
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Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu  
 70 75 80 85  
 caa agc tct gtt ctg gat gcc gat tat gtg acc ttg tct tcc ctg gat 403  
 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp  
 90 95 100  
 ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451  
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His  
 105 110 115  
 aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499  
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr  
 120 125 130  
 tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547  
 Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val Asp Glu Leu Asp Arg  
 135 140 145  
 cca gca atc cgc ttg gtg tcc tgg atc gcg ccg aca tct taagggtgcc 596  
 Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro Thr Ser  
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 gggctttaaa gtg 609

<210> 1150  
 <211> 162  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1150  
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 Trp Leu Val Thr Asn Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile  
 35 40 45  
 Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser  
 50 55 60  
 Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe  
 65 70 75 80  
 Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr  
 85 90 95  
 Leu Ser Ser Leu Asp Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln  
 100 105 110  
 Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe  
 115 120 125  
 Glu Ile Ser Arg Thr Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val  
 130 135 140  
 Asp Glu Leu Asp Arg Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro  
 145 150 155 160

Thr Ser

&lt;210&gt; 1151

&lt;211&gt; 1590

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1567)

&lt;223&gt; RXS00349

&lt;400&gt; 1151

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				Met	Leu	Ser	Phe	Ala	
				1				5	

acc	ctt	cgt	ggc	cgc	att	tca	aca	gtt	gac	gct	gca	aaa	gcc	gca	cct	163
Thr	Leu	Arg	Gly	Arg	Ile	Ser	Thr	Val	Asp	Ala	Ala	Lys	Ala	Ala	Pro	
				10					15						20	

ccg	cca	tcg	cca	cta	gcc	ccg	att	gat	ctc	act	gac	cat	agt	caa	gtg	211
Pro	Pro	Ser	Pro	Leu	Ala	Pro	Ile	Asp	Leu	Thr	Asp	His	Ser	Gln	Val	
			25					30					35			

gcc	ggt	gtg	atg	aat	ttg	gct	gcg	aga	att	ggc	gat	att	ttg	ctt	tct	259
Ala	Gly	Val	Met	Asn	Leu	Ala	Ala	Arg	Ile	Gly	Asp	Ile	Leu	Leu	Ser	
		40					45					50				

tca	ggt	acg	tca	aat	agt	gac	acc	aag	gta	caa	gtt	cga	gca	gtg	acc	307
Ser	Gly	Thr	Ser	Asn	Ser	Asp	Thr	Lys	Val	Gln	Val	Arg	Ala	Val	Thr	
	55					60					65					

tct	gcg	tac	ggt	ttg	tac	tac	acg	cac	gtg	gat	atc	acg	ttg	aat	acg	355
Ser	Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp	Ile	Thr	Leu	Asn	Thr	
70					75					80					85	

atc	acc	atc	ttc	acc	aac	atc	ggt	gtg	gag	agg	aag	atg	ccg	gtc	aac	403
Ile	Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg	Lys	Met	Pro	Val	Asn	
				90					95					100		

gtg	ttt	cat	gtt	gta	ggc	aag	ttg	gac	acc	aac	ttc	tcc	aaa	ctg	tct	451
Val	Phe	His	Val	Val	Gly	Lys	Leu	Asp	Thr	Asn	Phe	Ser	Lys	Leu	Ser	
			105					110					115			

gag	gtt	gac	cgt	ttg	atc	cgt	tcc	att	cag	gct	ggt	gcg	acc	ccg	cct	499
Glu	Val	Asp	Arg	Leu	Ile	Arg	Ser	Ile	Gln	Ala	Gly	Ala	Thr	Pro	Pro	
		120					125					130				

gag	gtt	gcc	gag	aaa	atc	ctg	gac	gag	ttg	gag	caa	tcc	cct	gcg	tct	547
Glu	Val	Ala	Glu	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Gln	Ser	Pro	Ala	Ser	
		135				140					145					

tat	ggt	ttc	cct	gtt	gcg	ttg	ctt	ggc	tgg	gca	atg	atg	ggt	ggt	gct	595
Tyr	Gly	Phe	Pro	Val	Ala	Leu	Leu	Gly	Trp	Ala	Met	Met	Gly	Gly	Ala	
150					155					160					165	

gtt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt	643
Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe	
170 175 180	
att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag	691
Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys	
185 190 195	
ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg	739
Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr	
200 205 210	
ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag	787
Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu	
215 220 225	
atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca	835
Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala	
230 235 240 245	
ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg	883
Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro	
250 255 260	
gtg aca gca agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc	931
Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly	
265 270 275	
att gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat	979
Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His	
280 285 290	
gtc atg ttg cct gcc atg gag tcc gct gca gca cct aat tat tcg tct	
1027	
Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser	
295 300 305	
aca ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca	
1075	
Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala	
310 315 320 325	
gtg ggt tgt tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act	
1123	
Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr	
330 335 340	
gcg ctg atg ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc	
1171	
Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly	
345 350 355	
ccc gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt	
1219	
Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly	
360 365 370	
ggt ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att	
1267	
Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile	

375                      380                      385  
 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg  
 1315  
 Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met  
 390                      395                      400                      405  
 tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg  
 1363  
 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala  
 410                      415                      420  
 gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt  
 1411  
 Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly  
 425                      430                      435  
 gag tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac  
 1459  
 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr  
 440                      445                      450  
 cgt gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag  
 1507  
 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu  
 455                      460                      465  
 cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc  
 1555  
 Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe  
 470                      475                      480                      485  
 ggt aat aaa agg taaaaatcaa cctgcttagg cgt  
 1590  
 Gly Asn Lys Arg

&lt;210&gt; 1152

&lt;211&gt; 489

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1152

Met Leu Ser Phe Ala Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala  
 1                      5                      10                      15  
 Ala Lys Ala Ala Pro Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr  
 20                      25                      30  
 Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly  
 35                      40                      45  
 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln  
 50                      55                      60  
 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp  
 65                      70                      75                      80  
 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg  
 85                      90                      95

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn  
 100 105 110  
 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala  
 115 120 125  
 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu  
 130 135 140  
 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala  
 145 150 155 160  
 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val  
 165 170 175  
 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser  
 180 185 190  
 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly  
 195 200 205  
 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu  
 210 215 220  
 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile  
 225 230 235 240  
 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly  
 245 250 255  
 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu  
 260 265 270  
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu  
 275 280 285  
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala  
 290 295 300  
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr  
 305 310 315 320  
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile  
 325 330 335  
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe  
 340 345 350  
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala  
 355 360 365  
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
 370 375 380  
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala  
 385 390 395 400  
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
 405 410 415



Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala  
 420 425 430

Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro  
 435 440 445

Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe  
 450 455 460

Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys  
 465 470 475 480

Thr Asn Gln Arg Phe Gly Asn Lys Arg  
 485

<210> 1153

<211> 440

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (417)

<223> RXS03183

<400> 1153

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 Glu Ala Glu Ala Thr Ala Gly Lys Phe Glu Val Gln Pro Leu Val Gly  
 1 5 10 15

aaa gac ggc gtc ggc gta tcc acc ctt ggt ggc tac aac aac ggc atc 96  
 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile  
 20 25 30

aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc 144  
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
 35 40 45

atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca 192  
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
 50 55 60

cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240  
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80

cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288  
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95

cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336  
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110

gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384  
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
 115 120 125

gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca 437  
 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser

130 135 440

ttc

<210> 1154  
 <211> 139  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 1154  
 Glu Ala Glu Ala Thr Ala Gly Lys Phe Glu Val Gln Pro Leu Val Gly  
 1 5 10 15  
 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile  
 20 25 30  
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
 35 40 45  
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
 50 55 60  
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80  
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95  
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110  
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
 115 120 125  
 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser  
 130 135

<210> 1155  
 <211> 1212  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1189)  
 <223> RXC00874

<400> 1155  
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 tctgggttga tctcaccgcc gatgaaaagg acgatatgga atg agc att ggc caa 115  
 Met Ser Ile Gly Gln  
 1 5  
 cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163  
 His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp  
 10 15 20  
 aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211

Asn	Val	Asp	Ile	Val	Leu	Ser	Arg	Glu	Cys	Gly	Glu	Asn	Thr	Leu	Ala	
			25					30					35			
gta	gtg	cgc	atc	aac	aat	gcg	ctg	tat	cag	ttg	ttg	gtc	aat	gat	gat	259
Val	Val	Arg	Ile	Asn	Asn	Ala	Leu	Tyr	Gln	Leu	Leu	Val	Asn	Asp	Asp	
		40					45					50				
ggc	aaa	gat	gtt	ctc	aac	gac	cac	gta	gaa	gag	gtc	ggg	gag	agt	ttc	307
Gly	Lys	Asp	Val	Leu	Asn	Asp	His	Val	Glu	Glu	Val	Gly	Ala	Ser	Phe	
	55					60					65					
gga	gca	tgg	act	ggc	agc	tct	gct	ttt	ccc	att	ggc	cct	ttc	act	cca	355
Gly	Ala	Trp	Thr	Gly	Ser	Ser	Ala	Phe	Pro	Ile	Gly	Pro	Phe	Thr	Pro	
	70				75					80					85	
ctc	ggc	aca	gaa	caa	tcc	aat	agc	tct	ttc	atc	acc	gcc	gac	aat	aaa	403
Leu	Gly	Thr	Glu	Gln	Ser	Asn	Ser	Ser	Phe	Ile	Thr	Ala	Asp	Asn	Lys	
				90					95					100		
gcg	atc	gtg	aaa	tac	ttc	cgc	aaa	tta	gaa	tcc	ggg	caa	aac	ccc	gat	451
Ala	Ile	Val	Lys	Tyr	Phe	Arg	Lys	Leu	Glu	Ser	Gly	Gln	Asn	Pro	Asp	
			105					110					115			
gtg	gag	cta	att	tct	aaa	att	tcc	tcc	tgc	ccc	aac	atc	gcg	ccc	atc	499
Val	Glu	Leu	Ile	Ser	Lys	Ile	Ser	Ser	Cys	Pro	Asn	Ile	Ala	Pro	Ile	
		120					125					130				
ctg	ggg	ttt	tcc	tcc	gct	gag	atc	tcc	ggg	gct	aac	tac	acc	ctg	gtc	547
Leu	Gly	Phe	Ser	Ser	Ala	Glu	Ile	Ser	Gly	Ala	Asn	Tyr	Thr	Leu	Val	
	135					140					145					
atg	gcg	cag	cag	tac	gtt	cca	ggg	ttg	gat	ggc	tgg	tca	cac	gcg	ctg	595
Met	Ala	Gln	Gln	Tyr	Val	Pro	Gly	Leu	Asp	Gly	Trp	Ser	His	Ala	Leu	
	150				155					160					165	
act	act	acc	tct	ggc	agc	ttt	gca	gag	gat	gca	gaa	aag	atc	ggc	gaa	643
Thr	Thr	Thr	Ser	Gly	Ser	Phe	Ala	Glu	Asp	Ala	Glu	Lys	Ile	Gly	Glu	
				170					175					180		
gcc	acc	cgc	aat	gtt	cac	act	gct	ctt	gca	tcg	gcc	ttc	cct	act	cgg	691
Ala	Thr	Arg	Asn	Val	His	Thr	Ala	Leu	Ala	Ser	Ala	Phe	Pro	Thr	Arg	
			185					190					195			
gta	gtt	ccc	gta	gaa	gca	ctc	gcc	gat	gcg	ctc	act	acc	cgc	ctt	aat	739
Val	Val	Pro	Val	Glu	Ala	Leu	Ala	Asp	Ala	Leu	Thr	Thr	Arg	Leu	Asn	
		200					205					210				
gaa	cta	atc	tcc	caa	gca	ccc	gaa	atc	gcc	cgc	ttc	aaa	gaa	gca	gcc	787
Glu	Leu	Ile	Ser	Gln	Ala	Pro	Glu	Ile	Ala	Arg	Phe	Lys	Glu	Ala	Ala	
	215					220					225					
atc	gac	ctc	tac	caa	tcg	ttg	gaa	ggc	gaa	gcc	cac	atc	caa	cgc	atc	835
Ile	Asp	Leu	Tyr	Gln	Ser	Leu	Glu	Gly	Glu	Ala	His	Ile	Gln	Arg	Ile	
	230				235					240					245	
cac	ggg	gac	ctc	cac	ttg	ggg	cag	ctc	atc	aaa	acc	ccc	gaa	cgc	tac	883
His	Gly	Asp	Leu	His	Leu	Gly	Gln	Leu	Ile	Lys	Thr	Pro	Glu	Arg	Tyr	
				250					255					260		
atc	ctc	atc	gat	ttc	gaa	ggc	gaa	cct	gcc	cgc	cca	ctt	aat	caa	cga	931
Ile	Leu	Ile	Asp	Phe	Glu	Gly	Glu	Pro	Ala	Arg	Pro	Leu	Asn	Gln	Arg	

265                      270                      275  
 cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc 979  
 Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser  
 280                      285                      290  
  
 atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac  
 1027  
 Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn  
 295                      300                      305  
  
 gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa  
 1075  
 Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln  
 310                      315                      320                      325  
  
 gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc  
 1123  
 Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala  
 330                      335                      340  
  
 tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg  
 1171  
 Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala  
 345                      350                      355  
  
 gtc gaa agg ctt cta gac tagttagtta ctctgcgtca aac  
 1212  
 Val Glu Arg Leu Leu Asp  
 360

&lt;210&gt; 1156

&lt;211&gt; 363

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1156

Met Ser Ile Gly Gln His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys  
 1                      5                      10                      15  
  
 Ser His Thr Ile Asp Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly  
 20                      25                      30  
  
 Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu  
 35                      40                      45  
  
 Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu  
 50                      55                      60  
  
 Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile  
 65                      70                      75                      80  
  
 Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile  
 85                      90                      95  
  
 Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser  
 100                      105                      110  
  
 Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro  
 115                      120                      125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala  
 130 135 140  
 Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly  
 145 150 155 160  
 Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala  
 165 170 175  
 Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser  
 180 185 190  
 Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu  
 195 200 205  
 Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg  
 210 215 220  
 Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala  
 225 230 235 240  
 His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys  
 245 250 255  
 Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg  
 260 265 270  
 Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala  
 275 280 285  
 Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His  
 290 295 300  
 Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly  
 305 310 315 320  
 Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala  
 325 330 335  
 Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys  
 340 345 350  
 Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp  
 355 360